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01 001/001/4964-72
02 Sequence 21 Application 05/08/4054964
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APPLICATION NUMBER: PCT/GB96/01409  
 PRIOR APPLICATION DATA: GB 951909.5  
 APPLICATION NUMBER: GB 951909.5  
 ATORSEY/AGENT INFORMATION:  
 NAME: Crawford, Arthur R.  
 REGISTRATION NUMBER: 25,372-698  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-816-4000  
 ADDRESS: 131 base jette  
 INFORMATION FOR SEQ ID NO. 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 131 base pairs  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 ORGANISM: HUMAN  
 SEQUENCE TYPE: DNA (genomic)  
 DB: 91149A.6

Query Match Similarity: 18.14; Score 242.6; DB: 6; Length 1313;  
 Best Local Similarity: 56.64; Pred. No. 3,3e-59;  
 Matches: 603; Conservative: 0; Mismatches: 429; Indels: 33; Gaps: 7;

15 CACCAATCAATTCGGAATTCGACATCACTACACGACACGACGTCGACAGACAA 74  
 Db 47 CACCAATCAATTCGGAATTCGACATCACTACACGACACGACGTCGACAGACAA 106  
 Db 75 CAAATGATGATCTGCTGGTAACTGCTGATGATGATGATGATGATGATGATGAT 134  
 Db 107 CAAATGATGATCTGCTGGTAACTGCTGATGATGATGATGATGATGATGATGAT 166  
 Db 135 GAA-----TGACAGACAGAGTTCACATCTGATGATGATGATGATGATGATGATGAT 188  
 Db 167 CTACTCTACTACTACGACAGATGCTGGTATCTACTCTCTTCAACGCTCTGAGTAACAT 226  
 Db 189 TACTGAGATACAGACATGATCTGACCTGGTATCTGGTATCTGGTATCTGGTATCTGG 248  
 Db 227 GCTGACAGACAGACATGATCTGACCTGGTATCTGGTATCTGGTATCTGGTATCTGG 286  
 Db 249 GATGCTGATCCGGAATACAGAGACGCTGATGACGATACATCCCAATGATACAC 308  
 Db 287 GGTGGTCGTCGGAATCTTCCAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 337  
 Db 309 CATCATCACTACTGAT-----CAGAGATACCTGCTGCTGGATGATCTGCTGGCTGAG 365  
 Db 338 TATGCTGATCTGCTGACAGACATGCTGCTGATGATGATGATGATGATGATGATGAT 397  
 Db 366 TATCATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425  
 Db 398 AATCATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457  
 Db 426 CATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485  
 Db 458 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 517  
 Db 486 C-----CTGACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 542  
 Db 518 CGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 577  
 Db 543 AGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602  
 Db 578 TACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 637  
 Db 603 TCGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662  
 Db 638 ---CAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694  
 Db 663 CATTATGAGAGACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 722  
 Db 695 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754

723 TATCCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 782  
 Db 755 TACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 814  
 Db 783 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 842  
 Db 815 TATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868  
 Db 843 GACTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902  
 Db 869 GAACTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938  
 Db 903 GAA-----ACTTAATCTCTCAATGATGATGATGATGATGATGATGATGATGATGAT 959  
 Db 929 AACAGCTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 988  
 Db 960 CCGGACTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019  
 Db 988 CATGCTGCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1048  
 Db 1020 AGAGAGAGAAAGCTTTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064  
 Db 1049 ACGGAGAGAGATCAATCAATGATGCTGATCTTACTTACTTACTTACTTACTTACT 1093

RESULT 7  
 US-09-350-756-5  
 Sequence 5, Application US/09350756  
 GENERAL INFORMATION:  
 APPLICANT: U.S. Army Medical Research Institute for Infectious Diseases  
 APPLICANT: John S. Lee  
 APPLICANT: Jonathan P. Smith  
 APPLICANT: Michael D. Parker  
 APPLICANT: Leonard Smith  
 APPLICANT: Leonard Smith  
 APPLICANT: Leonard Smith  
 TITLE OF INVENTION: Botulinum Neurotoxin Vaccine  
 FILE REFERENCE: 003/124/SAP RD ID NO 9557,756  
 CURRENT FILING DATE: 1995-07-09  
 EARLIER APPLICATION NUMBER: US 60/092,416  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: Apple Macintosh Microsoft Word 6.0  
 SEQ ID NO: 1317  
 TYPE: DNA  
 ORGANISM: Artificial  
 OTHER INFORMATION: /note="synthetic sequence encoding botulinum neurotoxin"  
 US-09-350-756-5

Query Match Similarity: 18.14; Score 242.6; DB: 10; Length 1317;  
 Best Local Similarity: 56.64; Pred. No. 3,3e-59;  
 Matches: 603; Conservative: 0; Mismatches: 429; Indels: 33; Gaps: 7;

15 CACCAATCAATTCGGAATTCGACATCACTACACGACACGACGTCGACAGACAA 74  
 Db 47 CACCAATCAATTCGGAATTCGACATCACTACACGACACGACGTCGACAGACAA 106  
 Db 75 CAAATGATGATCTGCTGGTAACTGCTGATGATGATGATGATGATGATGATGAT 134  
 Db 107 CAAATGATGATCTGCTGGTAACTGCTGATGATGATGATGATGATGATGATGAT 166  
 Db 135 GAA-----TGACAGACAGAGTTCACATCTGATGATGATGATGATGATGATGATGAT 188  
 Db 167 CTACTCTACTACTACGACAGATGCTGGTATCTACTCTCTTCAACGCTCTGAGTAACAT 226  
 Db 189 TACTGAGATACAGACATGATCTGACCTGGTATCTGGTATCTGGTATCTGGTATCTGG 248  
 Db 227 GCTGACAGACAGACATGATCTGACCTGGTATCTGGTATCTGGTATCTGGTATCTGG 286  
 Db 249 GATGCTGATCCGGAATACAGAGACGCTGATGACGATACATCCCAATGATACAC 308  
 Db 287 GGTGGTCGTCGGAATCTTCCAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 337  
 Db 309 CATCATCACTACTGAT-----CAGAGATACCTGCTGCTGGATGATCTGCTGGCTGAG 365  
 Db 338 TATGCTGATCTGCTGACAGACATGCTGCTGATGATGATGATGATGATGATGATGAT 397  
 Db 366 TATCATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425  
 Db 398 AATCATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457  
 Db 426 CATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485  
 Db 458 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 517  
 Db 486 C-----CTGACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 542  
 Db 518 CGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 577  
 Db 543 AGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602  
 Db 578 TACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 637  
 Db 603 TCGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662  
 Db 638 ---CAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694  
 Db 663 CATTATGAGAGACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 722  
 Db 695 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754







Sequence 10, Application US/0928326

Patent No. US20010180491

GENERAL INFORMATION:

APPLICANT: George Sachs

TITLE OF INVENTION: Method and Compositions for the

TITLE REFERENCE: 11782 treatment of fasciculations

CURRENT APPLICATION NUMBER: US/09/288,326

CURRENT FILING DATE: 1999-04-08

SOFTWARE: Fast-Seq for Windows Version 3.0

SEQ ID NO 10

TYPE: DNA

ORGANISM: Clostridium botulinum

US-288-326-10

KEY Match

Query Match

Local 50.24; Pred. No. 6.6e-25;

Mismatches 396; Conservative 375; Indels 18; Gaps 3;

QY 20 ATATCAATCCGAAATCGACATCATCTCGATCGCTGCTCAAGACACAACTC 79

DB 20 ATATCAATCCGAAATCGACATCATCTCGATCGCTGCTCAAGACACAACTC 79

QY 80 TGTATCGATCGCTGATAGTGTCTAA-----GTGAGATACAGCGGTGTGAC 133

DB 80 TGTATCGATCGCTGATAGTGTCTAA-----GTGAGATACAGCGGTGTGAC 133

QY 1020 TATAGATCTTATAGTATGATCACTCAAAATATATATGTAGTAAATTTATGTC 3079

DB 1020 TATAGATCTTATAGTATGATCACTCAAAATATATATGTAGTAAATTTATGTC 3079

QY 134 TGAATCGACACATCTGAAATCGACTCTTCCTGACTCTATCATCGATCTATC 193

DB 134 TGAATCGACACATCTGAAATCGACTCTTCCTGACTCTATCATCGATCTATC 193

QY 0680 CAAATAGAAATCAATCAATTTATTTAATGAAATGTAATATGATGCAATTT 3139

DB 0680 CAAATAGAAATCAATCAATTTATTTAATGAAATGTAATATGATGCAATTT 3139

QY 194 AAAACGACGATCTGATCGATCGCTGATCTCGATCTCGATCTCGATCTCGATCT 253

DB 194 AAAACGACGATCTGATCGATCGCTGATCTCGATCTCGATCTCGATCTCGATCT 253

QY 3140 TAAAAATGCTATGTATATATATATATATATATATATATATATATATATATAT 3199

DB 3140 TAAAAATGCTATGTATATATATATATATATATATATATATATATATATATAT 3199

QY 3200 GAATTCCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAA 3250

DB 3200 GAATTCCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAA 3250

QY 314 TGAATCGACACATCTGATCGATCGCTGATCGATCGATCGATCGATCGATCGAT 373

DB 314 TGAATCGACACATCTGATCGATCGCTGATCGATCGATCGATCGATCGATCGAT 373

QY 3251 TAAATCTTATGAAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 3310

DB 3251 TAAATCTTATGAAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 3310

QY 374 GATCTGATCGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 433

DB 374 GATCTGATCGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 433

QY 3311 GAACTTACAGATCTCGAATATCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 3370

DB 3311 GAACTTACAGATCTCGAATATCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 3370

QY 434 AAGATCTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 490

DB 434 AAGATCTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 490

QY 3491 TAAATCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAA 3430

DB 3491 TAAATCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAA 3430

QY 551 GTGAGATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 610

DB 551 GTGAGATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 610

QY 611 AGT 670

DB 611 AGT 670

QY 3551 GAATATTTTGAATTAATTAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAA 3610

DB 3551 GAATATTTTGAATTAATTAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAA 3610

QY 671 AAGATTTAT 730

DB 671 AAGATTTAT 730

QY 731 TGAATCGACACATCTGATCGATCGCTGATCGATCGATCGATCGATCGATCGATCGAT 790

DB 731 TGAATCGACACATCTGATCGATCGCTGATCGATCGATCGATCGATCGATCGATCGAT 790

QY 3671 TAAATCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAACTTAA 3730

DB 3671 TAAATCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAACTTAA 3730

QY 791 TGAAGAAAG 799

DB 3731 TAAATATATG 3739

RESULT 13

US-10-051-952-1

Sequence 1, Application US/10051952

Patent No. US20010180491

GENERAL INFORMATION:

APPLICANT: Baker, Patricia

TITLE OF INVENTION: Methods of Administering Botulinum Toxin

TITLE REFERENCE: 11782 treatment of fasciculations

CURRENT APPLICATION NUMBER: US/051,952

CURRENT FILING DATE: 2002-01-17

SOFTWARE: Fast-Seq for Windows Version 3.0

SEQ ID NO 10

TYPE: DNA

ORGANISM: Clostridium botulinum

US-10-051-952-1

KEY Match

Query Match

Local 50.24; Pred. No. 6.6e-25;

Mismatches 394; Conservative 377; Indels 18; Gaps 3;

QY 20 ATATCAATCCGAAATCGACATCATCTCGATCGCTGCTCAAGACACAACTC 79

DB 20 ATATCAATCCGAAATCGACATCATCTCGATCGCTGCTCAAGACACAACTC 79

QY 80 TGTATCGATCGCTGATAGTGTCTAA-----GTGAGATACAGCGGTGTGAC 133

DB 80 TGTATCGATCGCTGATAGTGTCTAA-----GTGAGATACAGCGGTGTGAC 133

QY 134 TGAATCGACACATCTGAAATCGACTCTTCCTGACTCTATCATCGATCTATC 193

DB 134 TGAATCGACACATCTGAAATCGACTCTTCCTGACTCTATCATCGATCTATC 193

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DB 2733 CAATGATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2782

QY 194 AAGATCGACATCTGATCGATCGCTGATCTCGATCTCGATCTCGATCTCGATCT 253

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QY 2783 TAAATATCTGAT 2842

DB 2783 TAAATATCTGAT 2842

QY 254 GTATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 313

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QY 2843 GAATCTGAT 2893

DB 2843 GAATCTGAT 2893

QY 314 TGAATCGACACATCTGATCGATCGCTGATCGATCGATCGATCGATCGATCGAT 373

DB 314 TGAATCGACACATCTGATCGATCGCTGATCGATCGATCGATCGATCGATCGAT 373

QY 2894 TAAATCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAA 2953

DB 2894 TAAATCTTAACTTTTAACTGATATAGTCTTAACTTAACTTAACTTAACTTAA 2953

QY 374 GAATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 433

DB 374 GAATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 433

QY 434 AAGATCTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 490

DB 434 AAGATCTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 490

QY 3014 TTAATATCTGAT 3073

DB 3014 TTAATATCTGAT 3073

QY 491 AAGATTTAT 550

DB 491 AAGATTTAT 550

QY 551 GTGAGATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 610

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DB 3134 GTATATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 3193

QY 611 AGT 670

DB 611 AGT 670

QY 3194 GAAATTTTGAATTAATTAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAA 3253

DB 3194 GAAATTTTGAATTAATTAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAA 3253





Search completed: November 1, 2002, 08:17:24  
Job time : 87 secs

GenCore version 5.1.1.3

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OK nucleic - nucleic search, using sw model

Run on: November 1, 2002, 06:20:38 : Search time 3271 Seconds

(without alignments)

10307:574 Million cell updates/sec

Title: US-09-910-186A-7

Search score: 1.341

Sequence: 1 gattccatgctgcacaa.....ggacggatgatgaagattc 1341

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Sequences: 2479110 seqs, 127143825 residues

Total number of hits satisfying chosen parameters: 49592208

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Bestium Match 0%

Summary: 127143825 sequences

Database: 1 Pending\_Patents\_NW\_Main\*

1: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

2: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

3: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

4: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

5: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

6: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

7: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

8: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

9: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

10: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

11: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

12: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

13: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

14: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

15: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

16: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

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43: /csp2\_6/pdata/1/pna/US986\_COMB.seq\*

Pred. No. is the number of results predicted by chance to have a  
 match with the query sequence. The result is the number of results  
 and is derived by analysis of the total score distribution.

SYNOPSIS

Result	Score	Query	Length	DB ID	Description
1	1341	100.0	1341	14	US-09-910-186A-7
2	1339.4	98.9	1411	17	US-09-350-756-2
3	1324.4	98.8	1411	17	US-09-350-756-2
4	1324.4	98.8	1411	17	US-09-350-756-2
5	1313.4	98.4	1531	5	US-08-121-975A-6
6	1311.4	98.4	1531	5	US-08-121-975A-6
7	1311.4	98.4	1531	5	US-08-121-975A-6
8	1311.4	98.4	1531	5	US-08-121-975A-6
9	1311.4	98.4	1531	5	US-08-121-975A-6
10	1311.4	98.4	1531	5	US-08-121-975A-6
11	1311.4	98.4	1531	5	US-08-121-975A-6
12	1311.4	98.4	1531	5	US-08-121-975A-6
13	1311.4	98.4	1531	5	US-08-121-975A-6
14	1311.4	98.4	1531	5	US-08-121-975A-6
15	1311.4	98.4	1531	5	US-08-121-975A-6
16	1311.4	98.4	1531	5	US-08-121-975A-6
17	1311.4	98.4	1531	5	US-08-121-975A-6
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19	1311.4	98.4	1531	5	US-08-121-975A-6
20	1311.4	98.4	1531	5	US-08-121-975A-6
21	1311.4	98.4	1531	5	US-08-121-975A-6
22	1311.4	98.4	1531	5	US-08-121-975A-6
23	1311.4	98.4	1531	5	US-08-121-975A-6
24	1311.4	98.4	1531	5	US-08-121-975A-6
25	1311.4	98.4	1531	5	US-08-121-975A-6
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27	1311.4	98.4	1531	5	US-08-121-975A-6
28	1311.4	98.4	1531	5	US-08-121-975A-6
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31	1311.4	98.4	1531	5	US-08-121-975A-6
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36	1311.4	98.4	1531	5	US-08-121-975A-6
37	1311.4	98.4	1531	5	US-08-121-975A-6
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39	1311.4	98.4	1531	5	US-08-121-975A-6
40	1311.4	98.4	1531	5	US-08-121-975A-6
41	1311.4	98.4	1531	5	US-08-121-975A-6
42	1311.4	98.4	1531	5	US-08-121-975A-6
43	1311.4	98.4	1531	5	US-08-121-975A-6













```

MEDION TYPE: PC Compatible
COMPUTER: IBM PC compatible
FORMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: GENSCAN 1.0, Version #1.30
CURRENT APPLICATION DATA: Release #1.0
APPLICATION NUMBER: PCT/0987/15394
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E., 037
FIRM: 037-037
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: OPND-02304
TELEPHONE: (615) 397-6810
TELEX: (615) 397-6830
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
STRANDS: double
TYPE: nucleic acid
FEATURES:
MOLECULE TYPE: DNA (genomic)
NAME/KEY: COS
ORGANISM: Homo sapiens
Accession No.: U011523
Genebank Accession No.: F097-15394-45
Date Recd: March 1987
Host Locus Similarity: 22.5%
Restriction Enzyme Sites: 191
Matches: 959; Conservative: 0; Mismatches: 363; Indels: 0; Gaps: 0
Length: 1547;

```

[illegible]

RESULT 7

Sequence 43, Application US/08/04159  
Status: Granted  
Applicant: Williams, James A.  
Applicant: Thalley, Bruce S.  
Inventor: Thalley, Bruce S.  
Title of Invention: Multivolt V  
Title of Invention: Multivolt MS  
Number of Sequences: 82  
Correspondence Address: Carroll  
Street 210 Montgomery Street,  
City: San Francisco  
State: California  
Country: United States of America  
ZIP: 94104

COMPUTER READABLE FORM:  
NO  
COMPUTER FILE: 41K  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
HARDWARE: IBM PC  
DRAWING: YES  
PUBLICATION DATE: 1988-01-10  
PUBLICATION TYPE: PATENT

APPLICATION NUMBER: US/08/0704,159  
 FILING DATE: 08/07/04,159  
 CLASSIFICATION: 424  
 NAME: Injuria, Dolor  
 REGISTRATION NUMBER: 40,027  
 REFERENCE/DOCKET NUMBER: OPND-02304  
 TELEPHONE: (415) 705-8410  
 TELEFAX: (415) 397-8130  
 INVENTOR: JAMES A. CARROLL  
 ADDRESS: 230 Montgomery Street, Suite 2200  
 San Francisco, California 94104  
 SEQUENCE CHARACTERISTICS: 45;  
 LENGTH: 1547 base pairs  
 TYPE: nucleic acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic);  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: 108..1533  
 ORIGIN: 704..1535-45

Seq. Match 55.34; Score 741.2; Db 11; Length 1547;  
 Start Loca. Similarity 72.54; Pred. 8.3e-154;  
 Gaps 955; Conservative 0; Mismatches 363; Indels 0; Gaps 0;  
 10 ATGGCGCAAAATATACATATCGAAATATCATCTCAACCTGCTTACAA 69  
 204 AGCTTATATATATACGAAATTTATATATATATATATATATATAT 263  
 70 GACAACTATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129  
 264 GAT 333  
 130 GACTGATGACGACGACGCTTCAACCTGCTGCTGCTGCTGCTGCTG 189  
 324 GAGCTTATATATATATATATATATATATATATATATATATATAT 383  
 190 ATGACAT 249  
 380 ACTCAAAATACAGATATATATATATATATATATATATATATATAT 443  
 250 ATTCTGATTCGAAATACAGACGAGATATATATATATATATATAT 309  
 444 ATATGAT 503  
 310 AT 369  
 504 AT 563  
 370 ATTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429  
 564 ATATGAT 623  
 430 CTGGAAGATCTCTGATATATATATATATATATATATATATATATAT 489  
 624 AGAT 683  
 450 ACAT 549  
 684 AT 743  
 550 CTGGAAT 609  
 740 AGAGAT 803  
 610 GAT 669  
 804 GAT 863  
 670 GAT 729  
 864 GAT 923

QY 730 CTGATCTACACAGAGATATATATCTTCACTGCTGCTGCTGCTGCTG 289  
 DB 740 TTAATCTACACAGAGATATATATCTTCACTGCTGCTGCTGCTGCTG 293  
 QY 920 CTGAGAGAGATCTTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849  
 DB 930 CTGAGAGAGATCTTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853  
 QY 980 CTGAGAGAGATCTTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043  
 DB 990 CTGAGAGAGATCTTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047  
 QY 850 AAATACATCAACTACCGGACCTGCTATCGTGGTCAAAATTCATCT 909  
 DB 860 AAATACATCAACTACCGGACCTGCTATCGTGGTCAAAATTCATCT 913  
 QY 1040 AACTATCAATATATATATATATATATATATATATATATATATAT 1103  
 DB 1050 AACTATCAATATATATATATATATATATATATATATATATATAT 1107  
 QY 910 AACTCTCTCATCATGATGATCATCTACCTACGATTAAGAGATCT 969  
 DB 920 AACTCTCTCATCATGATGATCATCTACCTACGATTAAGAGATCT 973  
 QY 1104 AACTCTCAATATATATATATATATATATATATATATATATATAT 1163  
 DB 1114 AACTCTCAATATATATATATATATATATATATATATATATATAT 1167  
 QY 970 TCACTCTGAATCAGATGCTGCTATACCTACGATTAAGAGATCT 1029  
 DB 980 TCACTCTGAATCAGATGCTGCTATACCTACGATTAAGAGATCT 1033  
 QY 1164 TTAATCTCAATATATATATATATATATATATATATATATATATAT 1223  
 DB 1174 TTAATCTCAATATATATATATATATATATATATATATATATATAT 1227  
 QY 1030 AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089  
 DB 1040 AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1093  
 QY 1324 AAATCTTTTCTCTCTATATATGATCTGCTGCTGCTGCTGCTGCT 1283  
 DB 1334 AAATCTTTTCTCTCTATATATGATCTGCTGCTGCTGCTGCTGCT 1287  
 QY 1090 GATATGACAGACGACGACCTACTCTGCTGCTGCTGCTGCTGCTG 1149  
 DB 1100 GATATGACAGACGACGACCTACTCTGCTGCTGCTGCTGCTGCTG 1153  
 QY 1384 GATATGACAGACGACGACGATATGCTGCTGCTGCTGCTGCTGCT 1343  
 DB 1394 GATATGACAGACGACGACGATATGCTGCTGCTGCTGCTGCTGCT 1347  
 QY 1150 ACTTACGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1209  
 DB 1160 ACTTACGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1213  
 QY 1344 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1403  
 DB 1354 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1407  
 QY 1310 GAATACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1269  
 DB 1320 GAATACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1273  
 QY 1404 GATATGATGATGATGATGATGATGATGATGATGATGATGATG 1463  
 DB 1414 GATATGATGATGATGATGATGATGATGATGATGATGATGATG 1467  
 QY 1370 TACAACTGAACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1329  
 DB 1380 TACAACTGAACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1333  
 QY 1464 TTAATCTCAATATATATATATATATATATATATATATATATAT 1523  
 DB 1474 TTAATCTCAATATATATATATATATATATATATATATATATAT 1527  
 QY 1330 TA 1331  
 DB 1324 TA 1525

RESULT #  
 US-10-771-012-45  
 : Sequence 45: Application US/10271012  
 : GENERAL INFORMATION  
 : APPLICANT: Williams, James A.  
 : TITLE OF INVENTION: Multivalent Vaccine For Clostridium  
 : CORRESPONDENCE ADDRESS: 82  
 : STREET: 230 Montgomery Street, Suite 2200  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: United States of America  
 : ZIP: 94104  
 : NUMBER OF SEQUENCES: 82  
 : COMPUTER READABLE FORM:  
 : FILE NAME: US-10-771-012-45  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PictIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION NUMBER: US/10/271,012  
 : FILING DATE: 15-Oct-2002  
 : PRIORITY DATE: 15-Oct-2002  
 : PREVIOUS APPLICATION DATA:  
 : PREVIOUS APPLICATION NUMBER: US/08/0704,159





SEQUENCE CHARACTERISTICS:  
 LENGTH: 3876 base pairs  
 TYPE: nucleic acid  
 TOPOLOGY: linear double  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE KEY: CDS  
 LOCATION: 1..3873  
 US-08-704-159-41

Query Match 55.3%; Score 741.2; DB 11; Length 3876;  
 Best Local Similarity 72.5%; Fred. No. 1.3e193;  
 Matches 959; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

QY 10 ATGCGCAATCAATACCAATCCGAAATCTGACATATCATCTCCATGCTGGTACAA 69  
 DB 3554 ATGTTAT 2613  
 QY 70 GACCAATCATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129  
 DB 3614 GACCAATCATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2673  
 QY 130 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
 DB 3674 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2733  
 QY 1790 ATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249  
 DB 2534 ATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2793  
 QY 250 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309  
 DB 2794 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2853  
 QY 310 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 369  
 DB 2854 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2913  
 QY 370 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 429  
 DB 2914 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2973  
 QY 430 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489  
 DB 2974 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3033  
 QY 490 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549  
 DB 3034 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3093  
 QY 550 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609  
 DB 3094 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3153  
 QY 610 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669  
 DB 3154 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3213  
 QY 670 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729  
 DB 3214 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789  
 QY 730 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789  
 DB 3274 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3333  
 QY 790 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 849  
 DB 3334 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3393  
 QY 850 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 909

DB 3394 AAT 3453  
 QY 910 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 969  
 DB 3454 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3513  
 QY 970 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1029  
 DB 3514 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1089  
 QY 1010 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1089  
 DB 3574 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3633  
 QY 1090 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1149  
 DB 3634 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3693  
 QY 1150 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209  
 DB 3694 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3753  
 QY 1210 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1269  
 DB 3754 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3813  
 QY 1270 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1329  
 DB 3814 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3873  
 QY 1330 TA 1331  
 DB 3874 TA 3875

RESULT 11  
 US-10-271-012-41  
 Sequence 41, Application US/10271012  
 GENESIS 41, Application US/10271012  
 APPLICANT: Willioms, James A.  
 TITLE OF INVENTION: Bullidum Neutrocin  
 NUMBER OF SEQUENCES: 82  
 CORRESPONDENCE ADDRESS:  
 STREET: 220 Montgomery Street, Suite 2200  
 CITY: San Francisco  
 STATE: California  
 ZIP: 94104  
 COMPUTER READABLE FORM:  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Bullidum Neutrocin  
 CURRENT RELEASE: i1.0, Version #1.30  
 APPLICATION NUMBER: US/10271,012  
 FILING DATE: 15-Oct-2002  
 PUBLICATION DATE:  
 PUBLICATION NUMBER: US/08/704,159  
 ATTORNEY:  
 NAME: Ingolia, Diane E.  
 TELEPHONE: (415) 703-8410  
 TELEFAX: (415) 703-8410  
 INFORMATION:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3876 base pairs

TYPE: nucleic acid  
STRANDNESS: double  
SEQUENCE: 5' to 3'  
FEATURE: 1  
MOLECULE TYPE: DNA (genomic)

NAME/KEY: CDS  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-271-012-41

Query Match 55.3%; Score 741.2; DB 43; Length 3876;  
Best Local Similarity 72.24; Pred. No. 3,4e-192;  
Matches 95; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

0Y 10 ATGGCCCAAAATACAAATCCGAATCTGACAAATATATATCTGACCTGGTACAA 69  
DB 2554 ATGTTAAAT 2613  
0Y 70 GACACAACTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129  
DB 2614 GAT 2673  
0Y 130 GACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 273  
DB 2674 GACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 2793  
0Y 190 ACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATATAT 283  
DB 2794 ACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATATAT 2853  
0Y 250 ATGCTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 309  
DB 2854 ATGCTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATATAT 3093  
0Y 310 ATGCTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 369  
DB 2854 ATGCTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATATAT 3693  
0Y 370 ATGCTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 429  
DB 2914 ATGCTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATATAT 4293  
0Y 430 CTGGAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489  
DB 2974 CTGGAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5093  
0Y 490 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549  
DB 3034 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5093  
0Y 550 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609  
DB 3094 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6093  
0Y 610 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 669  
DB 3154 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6693  
0Y 670 GAG 729  
DB 3214 GAG 7293  
0Y 730 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 789  
DB 3274 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7893  
0Y 790 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 849  
DB 3334 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 8493  
0Y 850 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 909  
DB 3394 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9093

## RESULT 12

US-05-730-237-3  
Sequence 3, Application US/09730237  
APPLICANT: Walker, Patricia  
TITLE OF INVENTION: Methods of Treating Hyperhidrosis  
INVENTOR: Walker, Patricia  
CURRENT APPLICATION NUMBER: US/09730237  
CURRENT FILING DATE: 2000-12-05  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 3: Patent In Ver. 2.1  
LENGTH: 3876  
ORGANISM: *botulinum toxin*  
US-08-730-237-3

Query Match 54.9%; Score 736; DB 26; Length 3876;  
Best Local Similarity 72.24; Pred. No. 3,4e-192;  
Matches 95; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

0Y 10 ATGGCCCAAAATACAAATCCGAATCTGACAAATATATATCTGACCTGGTACAA 69  
DB 2554 ATGTTAAAT 2613  
0Y 70 GACACAACTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129  
DB 2614 GAT 2673  
0Y 130 GACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 273  
DB 2674 GACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 2793  
0Y 190 ACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATATAT 283  
DB 2794 ACTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATATAT 2853  
0Y 250 ATGCTGATGACAAATACAAATCTGACAAATATATATATATATATATATATATAT 309







QY 1203 ATGAGGATACAAAGACTACTCTGCATCTCCAAATGGTACTGAGAGAGTAAAG 1262  
 DB 3843 AGCTAAAGATTAAGAGATTTTGTAAAGATAGTGTATTAAGAGTAAGAG 3902  
 QY 1263 CAAATCGATCAACCAAGTAACTGGATTTGCAATTTGGAGTCTCCGAAAGAGAGGTG 1322  
 DB 3903 GAAACATATAGTCAATTTGGAGTATTTGGAGTATTTCTCTAAGAGAGAGGTG 3962  
 QY 1323 GACCGATATGAGAT 1339  
 DB 3963 GACTGATATATNCT 3979

## RESULT 15

PCT-US97-15394-43  
 Sequence 43, Application PC/US9715394  
 APPLICANT: Williams, James A.  
 APPLICANT: Thallier, Bruce S.  
 TITLE OF INVENTION: Bivalent Vaccine For Clostridium  
 TITLE OF INVENTION: Bivalent Vaccine For Clostridium  
 NUMBER OF SEQUENCES: 62  
 CORRESPONDENCE ADDRESS: Carroll  
 STREET: 220 Montgomery Street, Suite 2200  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94104  
 COMPUTER READABLE FORM:  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 FILE NAME: PCT-US97-15394-43  
 CURRENT APPLICATION NUMBER: PCT/US97/15394  
 FILING DATE: 09/10/97  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ingolia, Elaine S.  
 ADDRESS: 1000 California Street, Suite 1007  
 REFERENCE/JUNKY NUMBER: OPED-02304  
 TELEPHONE: (415) 705-8410  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: 2120 base pair  
 STRANDNESS: double  
 TOPOLOGY: linear  
 FEATURE: nucleic acid  
 DESCRIPTION: /name = "DNA"

Query Match  
 Best Local Similarity 48.4%; Score 652.6; DB 1; Length 1526;  
 Matches 910; Conservative 68.8%; Pseud 10.0%;  
 Mismatches 412; Indels 0; Gaps 0;  
 QY 10 ATGGCCCAATCAATCTCGAATGCGTCAATGATCTCTGAGCTGAGCTGATCA 69  
 DB 204 ATGTCTTAATTAATTAATAGGAAATTTTAATTAATTAATTAATTAATTA 263  
 QY 70 GAAACATGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129  
 DB 264 GATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 323  
 QY 130 GAACTGATGAAAG 189

PCT-US97-15394-43

DB 324 AAGCTTAAGTAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 383  
 QY 190 ACTCAATGATGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 249  
 DB 384 ACTCAATGATGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 443  
 QY 250 ATGCTATGCTGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 309  
 DB 444 ATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 503  
 QY 310 ATGCTATGCTGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 369  
 DB 504 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 563  
 QY 370 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429  
 DB 564 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 623  
 QY 430 CTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489  
 DB 624 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 683  
 QY 490 ACAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 549  
 DB 684 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 743  
 QY 550 CTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609  
 DB 744 GAAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803  
 QY 610 CAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669  
 DB 804 CAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863  
 QY 670 GAAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729  
 DB 864 AAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 923  
 QY 730 CTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789  
 DB 924 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 983  
 QY 790 CTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849  
 DB 984 CTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043  
 QY 860 AAATCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909  
 DB 1044 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1103  
 QY 910 ACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969  
 DB 1104 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1163  
 QY 970 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1029  
 DB 1164 CTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223  
 QY 1030 AAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089  
 DB 1224 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1283  
 QY 1090 GAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1149  
 DB 1284 GAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1209  
 QY 1150 ACTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1269  
 DB 1344 ACTGTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1329  
 QY 1210 GAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1463  
 DB 1404 AAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1463





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QY 408 TGTATCTTGGATCAACATCGGTGAGACATCTGATACATCAATCGTGGTCTT 467
DB 10059 CACGACGAGCTTTCAGACAGACAGACAGACAGACAGACAGACAGACAG 10128
DB 468 GGTACATACATCAATCAATCTGAGACATCTCAATCAATCTCAATCAATCA 517
DB 10129 CACGACGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 10178

RESULT 2
US-10-092-411A-1023/c
; Sequence 1023, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE REFERENCE: 012796-101
; CURRENT FILING DATE: 2002-03-07
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5676
; LENGTH: 2358
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-1029
; Query Match 2.4%; Score 32.6; DB 6; Length 2398;
; Best Local Similarity 5.7%; Pred. No. 4.3;
; Matches 68; Conservative 0; Mismatches 0; Gaps 0;
QY 369 GATCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 428
DB 703 CACGACATCGGTTCACATATATGTTGTCGATGCGGATGTCGATGACATAC 644
QY 429 CCGTACGACATCTGATGATGATGATGATGATGATGATGATGATGATGAT 488
DB 643 CATTGACATCTGTCTATATGATGATGATGATGATGATGATGATGATGATG 564
QY 489 GACAT 495
DB 583 TTACAT 577

RESULT 3
US-10-092-411A-1175/c
; Sequence 1175, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE REFERENCE: 012796-101
; CURRENT FILING DATE: 2002-03-07
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5676
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-1175

```

```

Query Match 2.4%; Score 32; DB 6; Length 1854;
Best Local Similarity 5.7%; Pred. No. 4.3;
Matches 77; Conservative 0; Mismatches 0; Gaps 0;
QY 183 CGGTGTATTCAGATCAAGACATCTCACTCACTCACTCACTCACTCACTCT 242
DB 880 CCGTACGACATCTGATGATGATGATGATGATGATGATGATGATGATGAT 821
DB 423 CTCATGATCTGATTCGACGACATCAAGACAGGAGGATGATGATGATGATG 302
DB 820 TCTCTATAGTGTATGATGATGATGATGATGATGATGATGATGATGATG 761
QY 303 ATACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 334
DB 760 ATTCAGACACACCTTCATCAGCTGCTACT 729

RESULT 4
US-10-092-411A-1915/c
; Sequence 1915, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE REFERENCE: 012796-101
; CURRENT FILING DATE: 2002-03-07
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5676
; LENGTH: 2835
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-1915
; Query Match 2.4%; Score 33; DB 6; Length 2835;
; Best Local Similarity 45.4%; Pred. No. 5.3;
; Matches 83; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 935 TGGTCACTTCAGACGACGACGACGACGACGACGACGACGACGACGACG 994
DB 1639 TGGTCACTTCAGACGACGACGACGACGACGACGACGACGACGACGACG 1560
QY 995 TATACACACGAGTCTTCAGACGACGACGACGACGACGACGACGACGACG 1054
DB 1979 TCAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1520
QY 1095 ATACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1102
DB 1319 ACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1472

RESULT 5
US-10-092-411A-1685/c
; Sequence 1685, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE REFERENCE: 012796-101
; CURRENT FILING DATE: 2002-03-07
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5676
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-1685

```







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FEATURE:
; OTHER INFORMATION: mutant #1, C-terminally truncated variant of
; OTHER INFORMATION: human endothelial differentiation G-protein
; OTHER INFORMATION: coupled receptor (GPCR) 1 (E801)
FEATURE:
; NAME/REV: CDS
; LOCUS: U0911
; OTHER INFORMATION: Mutant #1 human EDG1
; OTHER INFORMATION: Mutant #1 human EDG1
PCT-U092-1242-2

Query Match      224; Score 39.8; DB 1; Length 1012;
Best Local Similarity 46.4; Pseq. No. 13;
Matches 57; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Ov 315 CNACTCGATGAGATATCTGCTGGAGATCTCGATCGCGGTACCGGTATCTCTG 374
   62 CTACTCGACTATGATATCATGTCGGCATATACACTACGCGGAGACTGATATCG 121
   122 CCGCAGCAGGAGACGACCTTAACCTGACTCTGGTGTTCATCTCTCTCTCTCT 181
   182 TATCTCTGGAGACCTTCTCTCTGACGCTTGGAGACGACGAGATCTCGCG 241
   242 ACCCATCTATCTACGAGGTAACTCG 523
   523 TCTCTCTGGAGACCTTCTCTCTGACGCTTGGAGACGACGAGATCTCGCG 582
   582 ACCCATCTATCTACGAGGTAACTCG 270
   270 ACCCATCTATCTACGAGGTAACTCG 270

Search completed: November 1, 2002, 08:17:49
Database: 151 seqs
Database: 151 seqs

```







APPLICANT: THALLEY, BRUCE S.  
 FILING DATE: 16-MAR-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA: US 08/329,154  
 FILING DATE: 25-OCT-1994  
 PRIOR APPLICATION DATA: US 08/161,907  
 FILING DATE: 02-DEC-1993  
 PRIOR APPLICATION DATA: US 07/985,321  
 FILING DATE: 02-DEC-1992  
 PRIOR APPLICATION DATA: US 07/429,791  
 FILING DATE: 04-DEC-1992  
 ATORNEY/AGENT INFORMATION:  
 NAME: INGOLIA, DIANE E.  
 REGISTRATION NUMBER: 40,037  
 TELEPHONE: (415) 705-8410  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 INFORMATION FOR SEQ ID NO. 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 438 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGIN: 405-496A-23

Query Match 35.4%; Score 831.5; DB 2: Length 438;  
 Best Local Similarity 40.0%; Pred. No. 4,7e-57;  
 Matches 189; Conservative 81; Mismatches 150; Indels 37; Gaps 10;

4 KYSEELNLLNLYNNKNDLISGKGVYGVDELN--DKQFKLTSMSKIRVT 61  
 10 EYINNTLSLNTSLNLSHLLISRYASHLNGSKNVDPIDNNQLPLSSKIRVI 69  
 62 ONKQITFNYSYDSSVPSYIRIKYKNDGQIRKINNTYINNNNSGWSYSEKQNV 121  
 70 LANAIVNENSTNSWLLAPYFN--SISLNNYTIINNNNSGWSYSEKQNV 126  
 122 WLIDQKTSKVSFTNREDSKINHWPTFTNN--LNAWIKYINKELESNIDTQI 180  
 127 WLIDQTKQKVFYKISNDISINHWPTFTNNLNNLSKYSYINGLIDQKPSFL 186  
 181 REVYANGSIFLLKDDDKTQFPMKYVTSFVSWLSGNSKYSYINGLIDQKPS 240  
 187 ONHASINMFKDQKRYHAIWYIFNPLNMLEKELKDLDSNGSLDQPDQY 246  
 247 LOTYFTHMLDTPKQYVNVGIVGHTMGWAGPSVYTNITASS-----LIRQ 259  
 291 LMYNHYNPNAGKSTIKLKK-----DSPVGLFTSKYKNSKYINVOYLQI 291  
 292 ENFTIKNSGNSINDVIREVDYLDFFNNGHVVYIKYIKKKEKFLAFVSSD 331  
 300 TFKTITKASGN--KDNVANNKNNYINHWPTFTNNLNNLSKYSYINGLIDQ 357  
 352 EYVWIOKEDDQPT--TSQCLLFQKDEBTEDELGHRRFESVIVEYDFTCSK 410  
 355 NLSVNGVNSGKIDTNCNCK--HLDGNSNDGFTGTFGNVIA-----KLVA 407  
 411 WLKVKRYNNKIDGKQVDFKDEMS 440  
 408 WNSQNGRS--SVTLGWSGTFVDGNGS 435

RESULT 4  
 us-08-915-136-23  
 Sequence 23, Application US/0891536  
 General Information:  
 APPLICANT: KINK, JOHN A.

APPLICANT: THALLEY, BRUCE S.  
 FILING DATE: 16-MAR-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA: US 08/329,154  
 FILING DATE: 25-OCT-1994  
 PRIOR APPLICATION DATA: US 08/161,907  
 FILING DATE: 02-DEC-1993  
 PRIOR APPLICATION DATA: US 07/985,321  
 FILING DATE: 02-DEC-1992  
 ATORNEY/AGENT INFORMATION:  
 NAME: INGOLIA, DIANE E.  
 REGISTRATION NUMBER: 40,037  
 TELEPHONE: (415) 705-8410  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 INFORMATION FOR SEQ ID NO. 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 438 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGIN: 405-496A-23

Query Match 35.4%; Score 831.5; DB 4: Length 438;  
 Best Local Similarity 40.0%; Pred. No. 4,7e-57;  
 Matches 189; Conservative 81; Mismatches 150; Indels 37; Gaps 10;  
 4 KYSEELNLLNLYNNKNDLISGKGVYGVDELN--DKQFKLTSMSKIRVT 61  
 10 EYINNTLSLNTSLNLSHLLISRYASHLNGSKNVDPIDNNQLPLSSKIRVI 69  
 62 ONKQITFNYSYDSSVPSYIRIKYKNDGQIRKINNTYINNNNSGWSYSEKQNV 121  
 70 LANAIVNENSTNSWLLAPYFN--SISLNNYTIINNNNSGWSYSEKQNV 126  
 122 WLIDQKTSKVSFTNREDSKINHWPTFTNN--LNAWIKYINKELESNIDTQI 180  
 127 WLIDQTKQKVFYKISNDISINHWPTFTNNLNNLSKYSYINGLIDQKPSFL 186  
 181 REVYANGSIFLLKDDDKTQFPMKYVTSFVSWLSGNSKYSYINGLIDQKPS 240



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FILING DATE: 25-OCT-1984
PRIOR APPLICATION DATA: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA: US 07/429,791
APPLICATION NUMBER: 08/480,604
ATTORNEY/AGENT INFORMATION:
NAME: INCOLLA, DIANE E. 097
REFERENCE/DOCKET NUMBER: 01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
FILING DATE: 04-DEC-1992
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TOPOLGCT: Linear
MOLECULE TYPE: protein
US-09-910-186a-26
Query Match 35.4%: Score 831.5; DB 2; Length 462;
Best Local Similarity 40.0%; Freq. No. 5e-57;
Matches 180; Conservative 83; Mismatches 150; Indels 37; Gaps 10;
4 KYSEILNMLILRTKNNILIDUSGYAKGVYDQVLEN-DKQKFLFSSNKSIVT 61
34 EYKINKTILNMLATSESHILDSYASKNGVNDINQQLNLSKSIWI 93
62 QNNTIKRNSGVDSVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 121
94 LKAVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 150
122 WTLIDQIKGTSEVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 180
151 WTLIDQIKGTSEVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 210
181 RYVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 240
211 GHIDSNIMFLKQDQDTHRYNTKYNFKDLNKEIKQLDQNSGLKADPNY 270
241 LKAVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 300
270 LQYDQIKGTSEVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 323
291 LKAVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 351
324 TRFLNATNKN-KNTYNDKNTNNTYNTKRNKRLNGLNAGACVATLNLATQV 381
352 ELYWTDIQEVDQD-TYDQLFKDSESDTDLGLHRTVEGCVITFYDTSIK 410
382 NLGVYVNSKNSDQNTNKNEN-NLQDNDQNDLDTGTFQFNHTA-----KVASN 431
411 WTLATVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 440
432 WTNQSLERS-SKTLGSMREIFVDQNGE 459
RESULT 7
US-08-915-136-26
Sequence 26, Application US 08/91136
GENERAL INFORMATION:
APPLICANT: KING, JOHN A.
ATTORNEY/AGENT INFORMATION:
NAME: INCOLLA, DIANE E. 097
REFERENCE/DOCKET NUMBER: 01308
TELEPHONE: (415) 705-8410
FILING DATE: 04-DEC-1992
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TOPOLGCT: Linear
MOLECULE TYPE: protein
US-08-915-136-26
Query Match 35.4%: Score 831.5; DB 4; Length 462;
Best Local Similarity 40.0%; Freq. No. 5e-57;
Matches 180; Conservative 83; Mismatches 150; Indels 37; Gaps 10;
4 KYSEILNMLILRTKNNILIDUSGYAKGVYDQVLEN-DKQKFLFSSNKSIVT 61
34 EYKINKTILNMLATSESHILDSYASKNGVNDINQQLNLSKSIWI 93
62 QNNTIKRNSGVDSVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 121
94 LKAVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 150
122 WTLIDQIKGTSEVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 180
151 WTLIDQIKGTSEVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 210
181 RYVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 240
211 GHIDSNIMFLKQDQDTHRYNTKYNFKDLNKEIKQLDQNSGLKADPNY 270
241 LKAVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 300
270 LQYDQIKGTSEVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 323
291 LKAVATNMTNYSFWIRPKYKQNTNNGNSKYNQVSDQIQQLNLSKSIWI 351
324 TRFLNATNKN-KNTYNDKNTNNTYNTKRNKRLNGLNAGACVATLNLATQV 381
352 ELYWTDIQEVDQD-TYDQLFKDSESDTDLGLHRTVEGCVITFYDTSIK 410
382 NLGVYVNSKNSDQNTNKNEN-NLQDNDQNDLDTGTFQFNHTA-----KVASN 431
411 WTLATVFTKPKNDQIQNTWNTIKWNSQWKSISQNWII 440
432 WTNQSLERS-SKTLGSMREIFVDQNGE 459

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CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
COUNTRY CODE: 1  
COMPUTER REAGABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: SYSTEMS RELEASE 4.2 OS/MS-DOS  
CURRENT APPLICATION DATA: Version 4.1.30  
APPLICATION NUMBER: 05/08/915.136  
CLASSIFICATION:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480.604  
APPLICATION NUMBER:  
PRIOR APPLICATION NUMBER: 05/08/405.496  
FILING DATE: 16-MAR-1995  
FILING DATE:  
APPLICATION NUMBER: 05/08/329.154  
FILING DATE: 25-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 05/08/161.907  
FILING DATE: 02-DEC-1993  
APPLICATION NUMBER:  
PRIOR APPLICATION NUMBER: 05/07/985.321  
APPLICATION DATA:  
PRIOR APPLICATION NUMBER: 05/07/439.791  
FILING DATE: 31-OCT-1989  
FILING DATE:  
NAME: ANSOLIA, DIANE E.  
REGISTRATION NUMBER: 40,037  
REFERENCE/DOCKET NUMBER: OPFD-01763  
TELEPHONE NUMBER: 415-705-8410  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE INFORMATION:  
LENGTH: 1996 amino acids  
TYPE: amino acid  
POLYCLONAL LINEAR:  
MOLECULAR WEIGHT: 228,678  
MW: 08-915-136-28

Query Match: 35.4%; Score 831.5; DB 4; Length 1296;

Best Local Similarity 40.0%; Pred. No. 1.9e-56;  
Matches 180; Conservative 83; Mismatches 150; Indels 37; Gaps

4 KYNSEILNNTILNLRVYDNNLZDLSYGAKVEVVDGVEL--DKNQPKLTSSANSKIRVT 61

868 EYKNI:INTSILNRYESNHLIDLSRYASKINIGSKVNPDPIDKNQIQLPNUSSKIEVI 927

62 QNQNIIENSVFLDFSVSFQIRIPRYKNDGIQNIYHNEYTIINCNNNGWKYSIRGNRII 121

926 LKNAIYNSMVEFSTFWIRIPRYEN--SISLNNEYTIINCNNNSGNKXVSLNYGEII 984

122 WTLDINGKTKSVFFEYNIREDISSEINRWFFVTINN-LNNAKIYINGKLESNTDIKI 180

985 WLQDTQEIQRVVFKYSQMINISDYINRWIFVTITNNRLANSKIYINGPLIDQKPISNL 1044

181 REVIANCEIIPKIDGIDIDTQFIIMKYVSIPTWELSSQSNTEERYKTSYSEVLKDFWGNP 240

1045 GNIHASNNINFKIDGCRDTHRYIWIKNYFNLFORXELNEXEIKDLYDNQNSG:IKDPWGDY 1104

241 LMNKEYYMENAGNKNYSYILKK-----DSPVCELTSTRSKYQNSKYINRYADLYG 291

db 1105 LQYDKFYIMLNLYDPNKYYVDNVNNGIRGMYLKGPGRSVNTTNIILNSS-----LYRG 1157

292 EKFIPIRKNSOSINDOIVRKEDYILDOFFNUNQBWRYTYKYFKRBEEXLAPISDSD 351

006 1158 TPEIIRKASGN--KDN+VRNNDRVYINVVANKEVRLA/NASQAGVERILSALEIPDVG 1215

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US-09-913-136-28  
Sequence 26, Application US/08915136

7 FACULTY NO. 0230960  
; GENERAL INFORMATION:  
; ADDRESS, CITY, STATE, ZIP CODE

APPLICANT: KING, JOHN A.  
APPLICANT: THALLEY, BRUCE S.  
APPLICANT: DASHOW, NISCHA V.

APPLICANT: STANLEY, ALAN F.  
APPLICANT: FIRCH, JOSEPH R.  
APPLICANT: SEABORN, DONALD E.

TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND PREVENTION OF C. DIPHTHERIAE DISEASE

NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:

ADRESSES: MEDLEN & CARROLL, LLP  
STREET: 220 MONTGOMERY STREET, SUITE 2200

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Copied from 10910186 on 05-07-2004

352 ELVNTQKTRP-TQOLLKREBESDGLIGIVBESVFEKFCFK 410  
1216 NLSGVVMSKQWNTKNSCN-NLQDNKNDGIDGPNHNA-----KLVASN 1265  
411 KLVKWKPKPKPKLKGWNTKNSCN-NLQDNKNDGIDGPNHNA-----KLVASN 1265  
1266 NTRQIERS-SPFJCSWEIPVDGWS 1293

RESULT 11  
US-07-618-312A-2  
Patent No. 538540  
GENERAL INFORMATION: US/07/618312A  
APPLICANT: Romsos Dr. Andrew J  
APPLICANT: Romsos Dr. Michael A  
APPLICANT: Romsos Dr. Jeffrey J  
APPLICANT: Fairweather Dr. Neil F  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
STREET: 2200 Clarendon Boulevard,  
CITY: Arlington,  
STATE: Virginia,  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
APPLICATION NUMBER: US/07/618-312A  
FILING DATE: 19910516  
PRIORITY DATE: 19910516  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8926832.0  
FILING DATE: 28-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9006097.1  
FILING DATE: 17-MAR-1990  
NAME: Crawford M. Arthur R  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOC# INFORMATION: 10-51  
TELEPHONE: 0101 703 8750400  
TELEFAX: 0101 703 5283468  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match  
Best Local Similarity 32.2%; Evid. No. 1,2e-48  
Matches 44; Conservative 48; Identicals 43; Gaps 12;

14 INLRKNNLDSGVANVEYDVEL---NKKQPKLTSNNKLPYDQNNLTPN 69  
23 ILANDNDHDSIFNSNVTPEQALVPYNGK-AHLVNESEVYHAKNDIEY 81  
70 SVFQSVFSPHPIKPYDQNNLTHNITLNNKH-----SNKISFQNSHTPT 124  
87 DNFNFTVPLVYFVAFVSAHLQGTNHSISNNKISVNSVSKNNLWTL 141  
125 DNGKRGVPTNTRD-SENT-NRATFTYNN-LNNKTKTKNSLWFOITRE 182

142 KDSGEVQITFR-DLPKQFAYLANKRNVFITTMDLSGAMLNINOVLRMSHITGLQ 200  
183 VIANEIEITKLDIDRTQYTHMYKFSFVITLSQSHIERKIQSTSEYKADPNQML 242  
201 IEHNNITVILQDNNNNVTSLEKFLPKALPKHILKILTSYLSITLIGAPWNNL 260  
243 YKKEVTFQAKNSKILKKSQVPELGRSKYNSNINVDITGIEFTFKNS 302  
261 YDREYVILVASSKQVLKNTDPTLTHNFTSKNKNITVRELNGLAFITKTPN 320  
303 QGINDVLEKREYITLDFNLNQRVYTT---KPKKPEKKFLAPSSDELINITY 358  
378 NKTGKQV 378  
321 NEI-USVSPQFKL-TVSNHNEHVTGPKQNNALNLRILVGYNAGPLTKME 378  
359 IKEDGPTQV 418  
378 AVKELKLTYSKLVYDKNAS--LGLVGTI---NQIGNPDEILLASINWFMNLD 493  
439 KYKALGNSQTPHDEWT 439  
434 K---LGCWDFVPTDEWT 450

RESULT 12  
US-08-280-228-2  
Patent No. 5571694  
GENERAL INFORMATION: Application US/08280228  
APPLICANT: Romsos Dr. Andrew J  
APPLICANT: Romsos Dr. Michael A  
APPLICANT: Romsos Dr. Jeffrey J  
APPLICANT: Fairweather Dr. Neil F  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
STREET: 1100 No. 557184th Glebe Road  
CITY: Arlington,  
STATE: Virginia,  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
APPLICATION NUMBER: US/08/280,228  
FILING DATE: 25-JUL-1994  
PRIORITY DATE: 19940725  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/618,312  
FILING DATE: 17-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8926832.0  
FILING DATE: 28-JUN-1989  
NAME: Wilson, Mary J  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOC# INFORMATION: 1-163  
TELEPHONE: {703} 816-4000  
TELEFAX: {703} 816-4000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TOPOLOGY: linear



MOLECULE TYPE: protein

US-08-280-228-4

Query Match 25 34 Score 545 DB 1 Length 452;  
 Similarity 32.24; Pct ID 12e38;  
 Matches 142; Conservative 89; Mismatches 183; Indels 28; Gaps 12;

QY 14 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 70 SYVDFGVKVPKVKNDQONTNHEVITLQKNN---SNGKLSRGRNITL 124  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 82 DMNFTVPLKVKVASHLQVGTNETSISMKKSSGSSGVKQKNCITL 141  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 125 DINGKSGVFNVEDISYI NNKVFVITNN LNNAKVTINKLENDKOTRE 182  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 142 KDSGEVWITR-DLPKFNATLANKWVITITINDLSNKLINVLKASAITGLA 200  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 163 VIANGEITFLKDDIDDTQTKVTSFNTLSGSHIERKIQSVETLKQVNFILM 242  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 201 INEDNITLKDNNQNNQVSDINFAICPAKFNELNLTYSITFLKQVWGLER 260  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 243 IREYTFMAGNSYIKLKQSPVGLTERTKPMQNSYINFDITGKFIIRKNS 302  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 261 VDTETLTPVASSQVCLNTDMLYNAVSYTNKLNITVRLNGATLKRTYTN 320  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 303 QGINDQVKKEDYITDIFPLQKQVRVIT---KFKREKCLFAPISDSDELNTQ 358  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 321 NEI-DSFVSGSDFTL TVSNVNNHIVGPGMGNFNLRLVGNWAGPIYKNE 378  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 359 IREYTFMAGNSYIKLKQSPVGLTERTKPMQNSYINFDITGKFIIRKNS 302  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 379 AKVLQATVSLQLYDKDNAS--LGLVTH--NQI GNDPRLILASMYTFNLAD 433  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 419 KPVKLEKQNSPTPDEGMT 439  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69  
 QY 434 K---ILGQDNVFTPDGWT 450  
 DB 23 ILKLRKONKIDSGVAVKVVQVDEL---NNKQFKTSASNKVYQONHLEN 69

RESULT 14  
 US-08-280-228-4  
 REQUIREMENTS 4; Application US/08280228  
 PUBLI. NO. 551694  
 GENERAL INFORMATION:  
 APPLICANT: Markoff Dr. Andrew J  
 APPLICANT: Markoff Dr. Andrew J  
 APPLICANT: Clare Dr. Jeffrey J  
 APPLICANT: Fairweather Dr. Neil F  
 APPLICANT: Fairweather Dr. Neil F  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: 1100 MON VANDERBILT  
 CITY: Arlington  
 STATE: Virginia  
 ZIP: 22201-7114  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

1 COMPUTER: IBM PC compatible  
 2 OPERATING SYSTEM: PC-DOS/MS-DOS  
 3 SOFTWARE: Patent Release #1.0, Version #1.25  
 4 CURRENT RELEASE DATE: 05/08/280.228  
 5 FILING DATE: 25-JUL-1994  
 6 CLASSIFICATION: 435  
 7 PUBLICATION NUMBER: US 07/618,312  
 8 FILING DATE: 27-NOV-1990  
 9 APPLICATION DATE: 27-NOV-1990  
 10 PRIOR APPLICATION DATA:  
 11 ZIP: 02110-2804  
 12 CITY: Boston  
 13 STATE: Massachusetts  
 14 COUNTRY: USA  
 15 COMPUTER READABLE FORM DISK  
 16 OPERATING SYSTEM: IBM PC compatible  
 17 OPERATING SYSTEM: PC-DOS/MS-DOS  
 18 CURRENT RELEASE DATE: 05/08/280.228  
 19 APPLICATION NUMBER: US/08/468,381A  
 20 FILING DATE: 21-JUN-1996  
 21 PRIOR APPLICATION DATA:  
 22 APPLICATION NUMBER: 60/000,473  
 23 REGISTRATION NUMBER: 30,154  
 24 ATTORNEY AGENT INFORMATION:  
 25 NAME: Clark, Paul T.  
 26 TELEPHONE: 617/242-6906  
 27 TELEPHONE: 617/242-6906  
 28 TELETYPE: 200154/6906  
 29 INFORMATION FOR SEQ ID NO: 5:  
 30 SOURCE CHARACTERISTICS:  
 31 TYPE: amino acid  
 32 TOPOLOGY: linear  
 33 Molecule type: protein  
 34 US-08-468-381A-5  
 35  
 36 Query Match 25.38, Score 594, DB 1, Length 618;  
 37 Exact Local Similarity 32.04, Pct. Id. 26.38;  
 38 Matches 141; Conservative 69; Mismatches 183; Gaps 12;  
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Db 545 AVLEADATTISVLEKLEKOKMAS--LGLVGH--XGICNDPREDILASNNYFHELD 599  
 Qy 419 KFYNEKLEKONQFIPROESNT 439  
 Db 600 L----LUGCONFFPDESNT 616

Search completed. November 1, 2002, 08:17:44  
 300 time 10 secs

GenCore version 5.1.3  
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ON protein - protein search, using sw model

Run on: November 1, 2002, 08:17:28 - Search time 31 Seconds

(without alignments)  
196,854 Million cell updates/sec

Title: US-09-910-186a-8

Perfect score: 2350

Sequence: 1 MANKYSLNNILMLRYK.....YMLGCGNQVFKDZWE 410

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Sequences: 90412 seqs, 13863272 residues

Number of hits satisfying chosen parameters: 90412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 10%

Listing first 43 summaries

Database:

Published Applications AA\*

1: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
2: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
3: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
4: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
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8: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
9: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
10: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
11: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
12: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
13: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*  
14: /cgn2.6/prodata/2/pubaa/US88\_NEW\_PUB pep\*

Prod. No. is the number of seqs predicted by chance to have a  
score at least as good as the score of the result being printed.  
and is derived by analysis of the total score distribution.

SUMMARIES

Prod. No.	Score	Match	Length	DB ID	Description
1	831.5	36.4	1295	10 US-09-726-949A-1	Sequence 1, Appl
2	826.5	35.2	1225	10 US-09-726-949A-1	Sequence 9, Appl
3	823.5	34.8	1225	10 US-09-726-949A-1	Sequence 2, Appl
4	818	33.5	144	8 US-08-981-087A-2	Sequence 2, Appl
5	284.5	12.1	144	8 US-08-981-087A-2	Sequence 3, Appl
6	143.5	6.1	144	8 US-08-981-087A-2	Sequence 15, Appl
7	143.5	6.1	144	8 US-08-981-087A-2	Sequence 15, Appl
8	144	6.1	996	10 US-09-815-242-1251	Sequence 5231, Ap
9	144	6.1	1009	10 US-09-815-242-1251	Sequence 1244, Ap
10	137.4	5.1	1009	10 US-09-815-242-1251	Sequence 1244, Ap
11	121	5.1	609	10 US-09-815-242-1251	Sequence 13683, A
12	112.1	5.1	1421	10 US-09-94-154-133	Sequence 13, Appl
13	112.1	5.1	1421	10 US-09-94-154-133	Sequence 13, Appl
14	110.5	4.7	1095	10 US-09-801-266-192	Sequence 392, Ap
15	110	4.7	751	10 US-09-801-266-192	Sequence 280, Ap
16	110	4.7	841	10 US-09-815-242-1251	Sequence 1275, Ap
17	110	4.7	841	10 US-09-815-242-1251	Sequence 1275, Ap
18	110	4.7	841	10 US-09-815-242-1251	Sequence 11373, A
19	109.5	4.7	829	10 US-09-801-368-124	Sequence 324, App

20 109.5 4.7 1018 10 US-09-815-242-1251  
21 109.5 4.7 1018 10 US-09-815-242-1251  
22 108 4.6 1343 10 US-09-924-154-14  
23 107 4.6 347 10 US-09-816-028A-17  
24 107 4.6 347 10 US-09-816-028A-17  
25 107 4.6 492 10 US-09-727-178-21  
26 107 4.6 492 10 US-09-727-178-21  
27 105.3 4.3 438 10 US-09-815-242-1251  
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# ALIGNMENTS

RESULT 1  
US-09-726-949A-1  
Sequence 1, Application US/09726949A  
GENERAL INFORMATION: 886A  
APPLICANT: Allergan, Inc.  
APPLICANT: Lilo, Wei-Jen  
APPLICANT: Lilo, Wei-Jen  
APPLICANT: Steward, Lance E.  
TITLE OF INVENTION: NEUTROPHILS WITH ENHANCED TARGET  
FILE REFERENCE: 3612-10002.00  
CURRENT FILING DATE: 2000-11-29  
CURRENT APPLICATION NUMBER: US/09/726.949A  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
TITLE: US-09-726-949A-1  
ORGANISM: Clostridium botulinum

Query Watch 35.44; Score 831.5; DB 10; Length 1295;  
Best Local Similarity 40.0%; Prod. No. 6.1e-59;  
Matches 180; Conservative 83; Mismatches 136; Indeals 37; Gaps 10;

QY 4 KYNELNNILMLKQNLIDSGYGVATVQVDELN-DKNQFLKSNKRYVT 61  
DB 867 EYKNNKLNILKQNLIDSGYGVATVQVDELN-DKNQFLKSNKRYVT 126  
QY 62 ONKATFVYDVSFVSNRYPKYKQNTYINNYTNMKNKSGIKRPIRL 121  
DB 927 LKALYVNSFVSFWIKRPIKFTN---SLNENYTNMKNKSGIKRPIRL 983  
QY 122 LKALYVNSFVSFWIKRPIKFTN---SLNENYTNMKNKSGIKRPIRL 180  
DB 954 WLOQYQKQVKSVMHISYNNHIVNNKLNKRYVINGLQKDPKSNL 243  
QY 181 EYKNNKLNILKQNLIDSGYGVATVQVDELN-DKNQFLKSNKRYVT 126  
DB 1044 GNTASNNMFKLQDQKQVKSVMHISYNNHIVNNKLNKRYVINGLQKDPKSNL 400  
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[illegible]

RESULTS: 081-087A-1

Sequence 1. Application US0891087A

GRANTED: 08/08/1985

APPLICANT: ELDOR, Margaret J.

APPLICANT: MacLachline, Margaret L.

APPLICANT: Minton, Nigel

APPLICANT: Minton, Nigel

APPLICANT: Tibball, Richard W.

TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF

INVENTOR: MINTON, NIGEL

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON, VANDERHIVE P.C.

STREET: 100 No. 082002001304Aith Gleda Rd, 8th floor

CITY: NEW YORK

STATE: VA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: SYMBIOSIS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA: (08/981.087A)

APPLICANT NUMBER: 0891087A

PLANNING NUMBER: 0891087A

CLASSIFICATION: 424

PRIOR APPLICATION DATA: PCT/GB86/01405

PLING DATE: 12-JUN-1956

PRIOR APPLICATION DATA: 08 951/909.5

APPLICANT NUMBER: 08 951/909.5

PLING DATE: 12-JUN-1985

ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R

REFERENCE: DOCKET NUMBER: 127

REFERENCE: DOCKET NUMBER: 124-688

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-81-1100

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

US-08-981-087A-1

Query Match 31.7% Score 732: DB 8: Length 431

Similarity 35.7% Prod No. 1.2e-50;

Matches 18; Conservative 88; Mismatches 149; Indels

oy 3 NYKSTLNTLITLVKYNKNDLIDISGDSYGVNFVETLVNDKPKLSSLS

dbD 13 NLYLTKKNDLIDRYNKKIDISGDSYGVNFVETLVNDKPKLSSLS

oy 61 TQNTQTFNSVFLDSVSPHTPKYKNDQGLNYINLVTKMKNNKNSKWK

oy 73 KQNDIVYGVNFVETLVNDKPKLSSLS

dbD 120 ITWLDIDKNTGVNFVETLVNDKPKLSSLS

oy 130 ITWLDIDKNTGVNFVETLVNDKPKLSSLS

oy 179 DTRVNEVETLVNDKPKLSSLS

dbD 230 NLYLTKKNDLIDRYNKKIDISGDSYGVNFVETLVNDKPKLSSLS

oy 239 NLYLTKKNDLIDRYNKKIDISGDSYGVNFVETLVNDKPKLSSLS

Db 249 NYLKNRYLLNU-----LPTDKSI-----TNSLNTKNOGVRQVPHF 342  
 Qy 288 -----KLEGFYTRKNSQSTN-ODVYKSHYVLDFFPHNGVRQVTKYKFEKGL 341  
 Db 292 SNRLVYTGVTYIRKNSGDSNDGNYKVKOLAVINVDVSVLADISIAPEKII 351  
 Qy 343 FLAP-SDSDELANTIKETVRODPTYSOLLPHKDEESTDEILGLGHPHYTSVFEY 402  
 Db 352 KLYTNSNSGUGIIVH-----DSIGNCNCMFQNN--NOGNTGLLGH----- 394  
 Qy 403 KDFCISWYLAKEVYKFNKLNCQIPKDEWTE 440  
 Db 395 SNNLVASWYVTRK--TESNOCPSFKSRHGWGE 430

RESULT 5  
 US-08-981-087A-3  
 Sequence 3, Application US/08981087A  
 GENERAL INFORMATION:  
 APPLICANT: Elmore, Michael J.  
 APPLICANT: Murchline, Margaret L.  
 APPLICANT: Murchline, Nigel P.  
 APPLICANT: Paschall, Vladimir A.  
 APPLICANT: Titball, Richard W.  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHYE P.C.  
 STREET: 1100 No. US20020081304aith Glebe Rd. 8th floor  
 CITY: Arlington  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201-4741  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 SOFTWARE: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: 09/981.087A  
 FILING DATE: 27-MAY-1998

CLASSIFICATION: 424  
 PRIOR APPLICATION DATA: PCT/GB96/01409  
 FILING DATE: 12-JUN-1996  
 PRIORITY NUMBER: GB 9511909.5  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Crawford, Arthur R.  
 ADDRESS: 12-JUN-1995  
 REGISTRATION NUMBER: 25,127  
 REFERENCE/DOCKET NUMBER: 124-688  
 TELEPHONE: 703-816-4000  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 144 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

Query Match 13.54; Score 318; DB 8; Length 144;  
 Best Local Similarity 45.24; Pred. No. 1,4e-18;  
 Matches 61; Conservative 33; Mismatches 5; Gaps 3;  
 Db 13 NYKVKIKNSILDMYKNNKLDYCGYKAVYQVDEL--NKNKQPLKISSKSKV 60  
 Qy 13 NYLKKIKNSILDMYKNNKLDYSGYKAVYQVDEL----- 111  
 Db 13 NYLKKIKNSILDMYKNNKLDYSGYKAVYQVDEL----- 111

Qy 61 TONQNIPIFNSVFLDSFSEWIRPYKNDQYQNTINHEVITINOM--INSONKISIRHNS 119  
 Db 73 AADNSIIINRYGYSISFWALPYATN--KYNLNEVITIIDIDINNNSWALSLATNK 129  
 Qy 120 IIMTIDINGKTSV 134  
 Db 130 IIMTIDQTAGNOKL 144  
 RESULT 5  
 US-08-981-087A-3  
 Sequence 3, Application US/08981087A  
 GENERAL INFORMATION:  
 APPLICANT: Elmore, Michael J.  
 APPLICANT: Murchline, Margaret L.  
 APPLICANT: Murchline, Nigel P.  
 APPLICANT: Paschall, Vladimir A.  
 APPLICANT: Titball, Richard W.  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHYE P.C.  
 STREET: 1100 No. US20020081304aith Glebe Rd. 8th floor  
 CITY: Arlington  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201-4741  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 SOFTWARE: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: 09/981.087A  
 FILING DATE: 27-MAY-1998  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 FILING DATE: 12-JUN-1996  
 PRIORITY NUMBER: GB 9511909.5  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Crawford, Arthur R.  
 ADDRESS: 12-JUN-1995  
 REGISTRATION NUMBER: 25,127  
 REFERENCE/DOCKET NUMBER: 124-688  
 TELEPHONE: 703-816-4000  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 144 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

Query Match 12.11; Score 284.5; DB 8; Length 144;  
 Best Local Similarity 39.31; Pred. No. 6e-16;  
 Matches 59; Conservative 27; Mismatches 45; Gaps 4;  
 Qy 136 FPIKEDISVETSNFVITNN--LANKATIKNGLSENDHDIHVIANCEIPIKLD 194  
 Db 2 PNTQNTISDVKMKIVITINLNGLSRITINKNLIDENSLGAD-HVSONILPIV 61  
 Qy 193 GDIOTQDQIMKRTYSFPIKTSOSNIETKIKQSYETKATPQWPLANKVYKQVACN 254  
 Db 62 GND--TRVGRFKVYFQTEKLTIELSDPEPDSILAKPMGNYLNRVYKAL-- 118  
 Qy 255 KSYILKADKQSPVEILFRKYNQNSVIN 284  
 Db 111

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3b 119 -----LTMKSI-----TUNSNFLN 133
RESULT 6
US-08-981-087A-4
Sequence 11, Application US/0924154
Patent No. US20020127241A1
GENERAL INFORMATION:
APPLICANT: S.M. Kim L.
TITLE OF INVENTION: Anti-plasmodium Compositions and Methods of Use
CURRENT FILING DATE: 2001-08-07
CURRENT APPLICATION NUMBER: US/09/924154
PRIOR APPLICATION NUMBER: US 6/233,525
NUMBER OF SEQ IDS: 17
SOFTWARE: Patentin version 3.1
INVENTOR: Kim, S.M.
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REFERENCE/AGENT NUMBER: 372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-510-0000
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDNESS:
TOP/LOC: linear
US-08-981-087A-4
Query Match
Best Local Similarity 6.4%; Score 149.5; DB 10; Length 1086;
Matches 89; Conservative 66; Mismatches 133; Indels 141; Gaps 21:
QY 6 NSILNLIINLRVQD--NKLIQ-LSTGKRVYGVYGLKQVWKLKSKSKVPT 61
DQ 7 SKSLINDVLSIQEKNFIDTSLVEGKKIKEMKICVTDNPK--SNNCAPR 63
QY 62 QNNTVFNSTFSDVSPTRIPKPYKNDQNTDTHNYVTLINCKNSGMSK:RQNH 121
DQ 64 RIQICVNIILSENEHYI---YRDSINNF--KENLKAVKLSLNVQKHN--- 114
QY 122 NLLIDNGKTSVPEYTR--EGLSEYINRFVYITNLNNAKVIKLSLNDKD 179
DQ 115 -----ENSKLDQI-----RMFL-----D 130
QY 180 IRVANGELIKLQIDTDFQHNKYSFWELS-----QSIEH--- 221
DQ 131 YQDIIGRELTSL---NQDITQKQPKFIPNENNNKLSLDELNDELNKLAK 185
QY 222 --BRKLGSLYSIKQF-----AGNPLAKRYEYFWAGK 255
DQ 186 WAKRDELDEBRKQKNTDICKYFADEQYVWLEKSPQIDENVALPTL--R 243
QY 256 NSTLKADKQKPKYKQNSKQNTINRD--LYGTRF--IRKSNSSQNDQIVR 311
DQ 244 NTNENK-----NLIENKQYQNNVQKQKWFILSNHFNQVQIHSNIFK 296
QY 312 --KEDVITLDFNQKQWVYVITTKREKSL-----FLAPISDELNTQY 362
DQ 297 EXENRVDYIFGTLN---TEYTNCKEKLPENSAKYKAPNAPSFLYS--KEN 348
QY 363 DQPTQYQLLAKFK 376
DQ 349 DESSVFQCKTKSK 362

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYTE P.C.
STREET: 1100 NO 0820020810Aalth Glabe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/91.087A
APPLICATION NUMBER: US/08/91.087A
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US/0894/01409
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: US 6511909.5
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REFERENCE/AGENT NUMBER: 372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-510-0000
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDNESS:
TOP/LOC: linear
US-08-981-087A-4
Query Match
Best Local Similarity 6.3%; Score 149; DB 8; Length 143;
Matches 41; Conservative 28; Mismatches 65; Indels 20; Gaps 5:
QY 288 LYGRKTIKTRSSNSIN-NDYVKEDYTLDFPNQKQWVYVYKFKREKFLAP 346
DQ 8 LYTVQVIVIRKNSQIS-SINFNPAKLNIAIVDQVYKJADISIAIPKIKIR 67
QY 347 ISGDEALVNIQIETEDQPTQYQLLFAKDESDRIGLIGIRNFESSIVEEYK 406
DQ 68 TSNSNSLSQIYVY--DSLNCKTKMFOFN--NGSMIGLOFLH-----SNG 110
QY 407 CISMATKRYKPKYKALGNQKIPKDSQWTE 440
DQ 111 VASMTNINMKRN--TSSNGCFWFSIRSGWDE 142

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RESULT 8
US-08-981-087A-4
Sequence 12, Application US/09815242
Patent No. US20020091569A1
GENERAL INFORMATION:
APPLICANT: Hasebeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Kyskind, Judith W.
APPLICANT: Traskick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
APPLICANT: Hasebeck, Robert
CURRENT FILING DATE: 2001-03-21

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QY 199 RTQ-----FMKQSYFIR-----TELSONSIBERY-----KIGSYSEAD 235  
 DB 342 SQQQQHREYINNPNSHMSITNNSKVERKLNLSGQOTNQGHQIRFLMQ 401  
 QY 236 --FW--GNNPLATKRYEWMGNKNSYIKLKDSFVBLITRSKQWNSYINVL 288  
 DB 402 PLUKSQNPNHNETCISGNSNNNTVSNOSI--EVS--SNENDKNSNSRN 437

RESULT 15  
 US-09-881-752A-280  
 : Sequence 280, Application US/09881752A  
 : Protein name: US-09-881-752A  
 : GENERAL INFORMATION  
 : APPLICANT: Meanthous, Harold  
 : APPLICANT: Al Garsell, Neal  
 : APPLICANT: Tom, Jean-Francois  
 : APPLICANT: Omen, Raymond P.  
 : TITLE OF INVENTION: Identification of Polypeptides  
 : FILE OF INVENTION: Encoding No. US2002015078Aa1 Helicobacter Polypeptides in the  
 : FILE REFERENCE: 06132/041002/us/09/481.752A  
 : PRIOR FILING DATE: 2001-06-15  
 : PRIOR APPLICATION NUMBER: US 08/833,457  
 : NUMBER OF SEQ ID NOS: 370  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : TYPE: PRT  
 : LENGTH: 251  
 : ORGANISM: Helicobacter pylori  
 : US-09-881-752A-280

Copy Match 4.78; Score 110, DB 10; Length 751;  
 : Local similarity 15.84; Score 0.24;  
 : Gaps 94; Conservative 76; Mismatches 162; Idents 226; Gaps 25;

DB 20 KNNLLDLSQGANVGVDELVDNDNQFUTLSANSKIATQNGII----- 67  
 DB 229 RUKNLFP-----EVEHNTIKA--KEIK-----DNKRVANDEKALLDRKIKITWC 276  
 DB 66 -----SNVFLDSV-----EHWIRPKYND-----GIQVJHN--EYTLNOM 105  
 DB 277 ILERNQATNKNNSILACSSIALKYQAFKEKNDLKAIAIFVSAEETDLEE 136  
 DB 106 KNSQWIKSTQNR--LIMTLIDNCKSVFENFVATDSIEYINRHFVFNGLNNA 163  
 DB 337 NNSACRLD--KSSDLEGADLYNGN-----EWSFSDSQKFSQYKDLQMKR 389  
 DB 164 KYINGKLENTDIDTRVYANGNEIIFLDDIDIDPTM---MKYSIFNLSQSN 219  
 DB 389 KI-----DLWVYV---MFLGDTATLTLMDVMTKYLIGLQAFRAK 431  
 DB 220 IERYK-----IGSYETLQDQNPMLNKEY 247  
 DB 432 ILGSVTHNIVCFDELQDQNALMFGWKDAQIALRYEYTLGTTN---NEY 487  
 DB 248 Y-----MFNAGNNNSYKL-----KQSPVGEILT 272  
 DB 488 ESYGLKALTEPFAKFTVSGKQKQFIIKFKIKLNTLSFNFRADTIN--P 544  
 DB 273 RKYNQNSYINPOLYGERFATKRNQSGINDIV----- 310  
 DB 545 RPDQVQSYILDFVNSRK-----GQWKEI--NDL--PIEELKQVEWIDVLANJHE 599  
 DB 311 -----KREYI--VLDFNLDNRKRYVITYKFKEEK 341  
 DB 600 FAKHWEIQLQVKTKEPILNNSIIELRNKDLMGFTNKQQRVHAHYQDTHGKE- 658  
 DB 342 LFLAPISDSKSEYVWFCRKEHQDQVYSCOLLFKQKRESDTGELGIRHYEYSIVFE 401

DB 655 -----EFQNIENRNLNEKAYS-----FMQAFAGGIESFSOT-----EPPAIEE 701  
 QY 402 YVDYFCTSYKYLKEWKEK 439  
 DB 702 KESNFGNSRY--QEWKEK 718

Search completed: November 1, 2002, 08:24:23  
 Job time : 34 secs

GenCore version 5.1.3

GenCorp version 3.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

CM protein - protein search, using sv model

Run on: November 1, 2002, 07:20:38 : Search time 291 seconds

run on: NOVEMBER 1, 2002, 07:20:36 ; SEARCH LINE 291 seconds  
(without alignments)  
974.854 Million cel updates/sec

Title: US-09-910-186A-B

Perfect score: 2350

sequence: I MANKYINSEILNNIILNDRK.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 4569744 8

100

total number of hits satisfying cho

Minimum D8 seg length: 0

Maximum DB seq length: 200000000

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Processing: Minimum March 04
Maximum March 1004
Listing first 45 summaries

Reading Filesets All-Wgns...
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2: /csp2_6/prodata1/paa/rs0806_COMP.psp
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4: /csp2_6/prodata1/paa/rs0808_COMP.psp
5: /csp2_6/prodata1/paa/rs0809_COMP.psp
6: /csp2_6/prodata1/paa/rs0810_COMP.psp
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18: /csp2_6/prodata1/paa/rs0822_COMP.psp
19: /csp2_6/prodata1/paa/rs0823_COMP.psp
20: /csp2_6/prodata1/paa/rs0824_COMP.psp
21: /csp2_6/prodata1/paa/rs0825_COMP.psp
22: /csp2_6/prodata1/paa/rs0826_COMP.psp
23: /csp2_6/prodata1/paa/rs0827_COMP.psp
24: /csp2_6/prodata1/paa/rs0828_COMP.psp
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39: /csp2_6/prodata1/paa/rs0843_COMP.psp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No	Score	k	Match	Length	DB	SUMMARIES	
						Query No	Description
1	230	100	0	440	3	US	Sequence 8, April
2	230	100	0	440	3	US	Sequence 16, April
3	240	95	5	472	1	PO	Sequence 46, April
4	240	95	5	472	1	PO	Sequence 46, April
5	240	95	5	472	1	US	Sequence 46, April
6	240	95	5	472	1	US	Sequence 46, April
7	240	95	5	472	1	US	Sequence 46, April
8	240	95	5	472	1	US	Sequence 46, April
9	240	95	5	472	1	US	Sequence 46, April
10	240	95	5	472	1	US	Sequence 46, April
11	240	95	5	472	1	US	Sequence 46, April
12	240	95	5	472	1	US	Sequence 46, April
13	240	95	5	472	1	US	Sequence 46, April
14	240	95	5	472	1	US	Sequence 46, April
15	240	95	5	472	1	US	Sequence 46, April
16	240	95	5	472	1	US	Sequence 46, April
17	240	95	5	472	1	US	Sequence 46, April
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25	240	95	5	472	1	US	Sequence 46, April
26	240	95	5	472	1	US	Sequence 46, April
27	240	95	5	472	1	US	Sequence 46, April
28	240	95	5	472	1	US	Sequence 46, April
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50	240	95	5	472	1	US	Sequence 46, April
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52	240	95	5	472	1	US	Sequence 46, April
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54	240	95	5	472	1	US	Sequence 46,

## ALIGNMENTS

RESULT 1  
US-09-611-419A-B  
GENERAL INFORMATION US/09611419A  
1  
2  
3  
4 APPLICANT: Smith, Leonard A.  
5  
6 APPLICANT: Smith, Leonard A.  
7  
8 APPLICANT: Middlebrook, John L.  
9  
10 APPLICANT: Leporello, Ruth.  
11  
12 APPLICANT: Middlebrook, John L.  
13  
14 APPLICANT: Brown, Douglas R.  
15  
16 TITLE OF INVENTION: DOMINANT VACCINE  
17  
18 TITLE OF INVENTION: DOMINANT VACCINE AGAINST BOVILINEN  
19  
20 FILE REFERENCE: A3636 007352 005  
21  
22 CURRENT APPLICATION NUMBER: US/09/611-419A  
23  
24 PENDING APPLICATION NUMBER: PGT/US00/12490  
25  
26 PRIOR FILING DATE: 2000-05-12  
27  
28 PRIOR APPLICATION NUMBER: 60/133-865  
29  
30 PRIOR FILING DATE: 1999-05-12  
31  
32 PRIOR APPLICATION NUMBER: 60/133-866  
33  
34 PRIOR FILING DATE: 1999-05-12  
35  
36 PRIOR FILING DATE: 1999-05-12  
37  
38 PRIOR FILING DATE: 1999-05-12  
39  
40 PRIOR FILING DATE: 1999-05-12  
41  
42 PRIOR FILING DATE: 1999-05-12  
43  
44 PRIOR FILING DATE: 1999-05-12  
45  
46 PRIOR FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8  
 NAME: PPT-42  
 TYPE: PPT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 INFORMATION: Fused polypeptide of a synthetic construct based  
 ON OTHER INFORMATION: JONTS INC.  
 US-05-611-419A-8

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Query Match      100.0%; Score 2350; DB 20; Length 440;
Best Local Similarity 100.0%; Pred. No. 3e-206;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

## RESULT 2

08-99-910-186A-2  
 : Sequence B. Application US/09970186A

GENERAL INFORMATION:  
CREDIT/COUNT: 11 C Army Medical Department Command

**TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM**

FILE REFERENCE: A33525-A 067252-0107

: CURRENT FILING DATE: 2001-07-20

;; PRIOR APPLICATION NUMBER: PCT/US00/12890  
: PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: 09/611,419  
 ; EXPIRATION DATE: 2000-02-06

; PRIOR APPLICATION NUMBER: 60/133,865

: PRIOR APPLICATION NUMBER: 60/133,866

PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/133,867

; PRIOR FILING DATE: 1999-05-12  
 ; PRIOR APPLICATION NUMBER: 60/123 868

; PRIOR FILING DATE: 1999-05-12

PRIOR FILING DATE: 1999-05-12

PRIOR APPLICATION NUMBER: 00/153,673

PRIOR FILING DATE: 1998-08-12  
 PRIOR FILING DATE: 1998-09-21  
 PRIOR FILING DATE: 1999-05-11  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: SeqMan 4.0  
 SEQ ID NO: 8  
 LENGTH: 440  
 ORGANISM: Artificial Sequence  
 FEATURE: Synthetic construct based on Clostridium botulinum  
 OTHER INFORMATION: sequence

Query Match 100.00; Score 2350; DB 23; Length 440;

[illegible]

### RESULT 3

ACT-US97-15394-46  
Sequence 46: Application PC/TUS9715394

GENERAL INFORMATION:  
 ADDRESS: WILLIAMSON, TAMAR B

APPLICANT: Thalley, Bruce S.

TITLE OF INVENTION: Botulinum

NUMBER OR SEQUENCE OF  
CORRESPONDENCE ADDRESS:

ADDRESS: Neulen & Carroll  
 SUITE: 220 Montomery Street, Suite 2200

CITY: San Francisco

COUNTRY: United States of America

COMPUTER READABLE FORM:

```

;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS  
COMPANIES: Patented Release #10

CURRENT APPLICATION DATA:



COUNTRY: United States of America  
 ZIP: 31-04  
 COMMUNICATOR: MACLES ROOM:  
 COMMUNICATOR: MACLES ROOM:  
 COMMUNICATOR: MACLES ROOM:  
 OPERATING SYSTEM: IBM PC compatible  
 CURRENT APPLICATION DATA: US/09/13-05, Version #1.30  
 APPLICATION NUMBER: US/09/271-012  
 TELEPHONE: (415) 705-4410  
 CLASSIFICATION: CONFIDENTIAL  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ingolia, Diane E.  
 REFERENCE/DOCKET NUMBER: 037  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-4410  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: SEQ ID NO: 46:  
 US-09-271-012-46  
 Query Match 93.63; Score 2140; DB 26; Length 472;  
 Best Local Similarity 99.54; Pred. No. 2.8e-05;  
 Matches 438; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 MANKYSEILNLLKLFKNNLIDSGYGAQVYDVELENKPKLTSSANSKIV 60  
 2 33 MEKTYNSVFLDSEYVSRIPKTKDQNTINMETIINCKMNSGKISIGRI 120  
 3 61 TQNMITFNSVFLDSEYVSRIPKTKDQNTINMETIINCKMNSGKISIGRI 152  
 4 93 TQNMITFNSVFLDSEYVSRIPKTKDQNTINMETIINCKMNSGKISIGRI 180  
 5 121 IWLIDNKTYSVFEVHEDISYINMHPVITNNLNNAIYINCKLESNTIKI 210  
 6 153 IWLIDNKTYSVFEVHEDISYINMHPVITNNLNNAIYINCKLESNTIKI 240  
 7 181 REVANKEIYKFLQDIDRTQNTKNTKTSVFNPSVITNNLNNAIYINCKLESNTIKI 270  
 8 213 REVANKEIYKFLQDIDRTQNTKNTKTSVFNPSVITNNLNNAIYINCKLESNTIKI 300  
 9 241 LNNKNTYVFNAGNSYKTKKSGVPELTSTKNSQNTINVDLTGKTIKRS 330  
 10 273 LNNKNTYVFNAGNSYKTKKSGVPELTSTKNSQNTINVDLTGKTIKRS 360  
 11 301 NSGSDINDVAVKDYIYDFPNLNQENWVYTKYFKKEKFLAPISDSSEYNTQIK 390  
 12 333 NSGSDINDVAVKDYIYDFPNLNQENWVYTKYFKKEKFLAPISDSSEYNTQIK 420  
 13 361 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 450  
 14 393 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 480  
 15 421 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 510  
 16 453 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 540

RESULT 6

US-08-123-975a-2  
 GENERAL INFORMATION US/08123975a  
 APPLICANT: Middlebrook, John L  
 APPLICANT: Lafontiere, Hugh F

APPLICANT: Clayton, Michael A  
 APPLICANT: Brown, Douglas R  
 APPLICANT: Brown, Douglas R  
 TITLE OF INVENTION: SUBSTITUTES FOR FUSION PRODUCT AS VACCINE  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 CORRESPONDENCE ADDRESS:  
 CORRESPONDENCE ADDRESS:  
 STREET: Off of Command Jdg, Adv.  
 CITY: Fredrick  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 21702-5012  
 COMMUNICATOR: MACLES ROOM:  
 COMMUNICATOR: MACLES ROOM:  
 COMMUNICATOR: MACLES ROOM:  
 OPERATING SYSTEM: IBM PC compatible  
 CURRENT APPLICATION DATA: US/09/123-975a  
 APPLICATION NUMBER: US/09/123-975a  
 TELEPHONE: (301) 613-7165  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heddicks, Glenn  
 REFERENCE/DOCKET NUMBER: mid.1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 613-7165  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: N-terminal  
 ORGANISM: Heavy chain of serotyp B botulinum toxin  
 US-08-123-975a-2  
 Query Match 93.64; Score 2140; DB 5; Length 850;  
 Best Local Similarity 99.54; Pred. No. 6.6e-05;  
 Matches 438; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 MANKYSEILNLLKLFKNNLIDSGYGAQVYDVELENKPKLTSSANSKIV 60  
 2 411 MANKYSEILNLLKLFKNNLIDSGYGAQVYDVELENKPKLTSSANSKIV 120  
 3 61 TQNMITFNSVFLDSEYVSRIPKTKDQNTINMETIINCKMNSGKISIGRI 150  
 4 93 TQNMITFNSVFLDSEYVSRIPKTKDQNTINMETIINCKMNSGKISIGRI 180  
 5 121 IWLIDNKTYSVFEVHEDISYINMHPVITNNLNNAIYINCKLESNTIKI 210  
 6 153 IWLIDNKTYSVFEVHEDISYINMHPVITNNLNNAIYINCKLESNTIKI 240  
 7 181 REVANKEIYKFLQDIDRTQNTKNTKTSVFNPSVITNNLNNAIYINCKLESNTIKI 270  
 8 213 REVANKEIYKFLQDIDRTQNTKNTKTSVFNPSVITNNLNNAIYINCKLESNTIKI 300  
 9 241 LNNKNTYVFNAGNSYKTKKSGVPELTSTKNSQNTINVDLTGKTIKRS 330  
 10 273 LNNKNTYVFNAGNSYKTKKSGVPELTSTKNSQNTINVDLTGKTIKRS 360  
 11 301 NSGSDINDVAVKDYIYDFPNLNQENWVYTKYFKKEKFLAPISDSSEYNTQIK 390  
 12 333 NSGSDINDVAVKDYIYDFPNLNQENWVYTKYFKKEKFLAPISDSSEYNTQIK 420  
 13 361 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 450  
 14 393 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 480  
 15 421 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 510  
 16 453 EYDQPTQYKQLPKFQDSEDTGLGIGHRTSGICWVEYKTCYSINLAKYKSP 540

OY 421 YNKLGNQWTFPDEWTE 440  
 DB 831 YNKLGNQWTFPDEWTE 850  
 RESULT 7  
 US-09-831-050-4  
 TITLE OF INVENTION: Application US/0981050  
 GENERAL INFORMATION:  
 APPLICANT: SHONE, Clifford Charles  
 INVENTOR: SHONE, Clifford Charles  
 APPLICANT: HALLIS, Bassam  
 APPLICANT: SILMAN, Nigel  
 CURRENT APPLICATION NUMBER: US/0981050  
 CURRENT FILING DATE: 1999-11-05  
 PRIOR FILING DATE: 1998-11-05  
 NUMBER OF SEQ IDS NOS: 11  
 SOFTWARE: Patent In Ver. 2.1  
 SEQ ID NO 7  
 LENGTH: 1070  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 SEQUENCE INFORMATION: Description of Artificial Sequence: construct  
 US-09-831-050-4

Query Match 99.64; Score 2340; DB 22; Length 1070;  
 Best Local Similarity 99.54; Pred. No. 9,3e-205; Identals 0; Gaps 0;  
 Matches 438; Conservative 0; Mismatches 2; Indels 0  
 OY 61 1 MANKYSEILNIIILKRTKDNKLDLSGAKVYDVGVDELNKNKQFLTSSANSKIRV 60  
 DB 631 MANKYSEILNIIILKRTKDNKLDLSGAKVYDVGVDELNKNKQFLTSSANSKIRV 630  
 OY 691 TONONTNPNVDFSVFWRPKYKNDGIONTHRETTINMKNNSDKISIGNR 120  
 DB 691 TONONTNPNVDFSVFWRPKYKNDGIONTHRETTINMKNNSDKISIGNR 120  
 OY 121 IWLIDNKNSTKSVFVFNEDISYINMFWFVITNNANNTYINKNLESTNID 180  
 DB 751 IWLIDNKNSTKSVFVFNEDISYINMFWFVITNNANNTYINKNLESTNID 180  
 OY 181 REVANKEIFKLDIDTDFNMKYSIFMTELSGNSIERKYSISETYKLPMPN 240  
 DB 811 REVANKEIFKLDIDTDFNMKYSIFMTELSGNSIERKYSISETYKLPMPN 240  
 OY 241 LMKNTYTFMAGNKSITKADKSPVGLTRKYNKNSKYNVDTLCEKTFIRKS 300  
 DB 871 LMKNTYTFMAGNKSITKADKSPVGLTRKYNKNSKYNVDTLCEKTFIRKS 300  
 OY 301 NSGQNDQVYKEDYTLDFNNQKRWYTYKFKKEKFLAPISDSSELYNTQIK 360  
 DB 931 NSGQNDQVYKEDYTLDFNNQKRWYTYKFKKEKFLAPISDSSELYNTQIK 360  
 OY 361 EYDQTFQKQIFKDESDTDLGIGHRTFSGVYKVKYKFLAPISDSDEFYTIQIK 420  
 DB 991 EYDQTFQKQIFKDESDTDLGIGHRTFSGVYKVKYKFLAPISDSDEFYTIQIK 420  
 OY 421 YNKLGNQWTFPDEWTE 440  
 DB 1051 YNKLGNQWTFPDEWTE 1070

RESULT 8  
 US-09-831-050-7  
 Sequence 7, Application US/0981050  
 GENERAL INFORMATION:  
 APPLICANT: SHONE, Clifford Charles  
 INVENTOR: SHONE, Clifford Charles  
 APPLICANT: SUTTON, John Mack  
 APPLICANT: HALLIS, Bassam

APPLICANT: SILMAN, Nigel  
 TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells  
 FILE REFERENCE: 1581.0800000  
 CURRENT FILING DATE: 1999-11-05  
 PRIOR APPLICATION NUMBER: PCT/GB99/03659  
 PRIOR FILING DATE: 1998-11-05  
 NUMBER OF SEQ IDS NOS: 21  
 SOFTWARE: Patent In Ver. 2.1  
 SEQ ID NO 7  
 LENGTH: 1095  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 SEQUENCE INFORMATION: Description of Artificial Sequence: Construct  
 US-09-831-050-7  
 Query Match 99.64; Score 2340; DB 22; Length 1095;  
 Best Local Similarity 99.54; Pred. No. 9,6e-205; Identals 0; Gaps 0;  
 Matches 438; Conservative 2; Mismatches 2; Indels 0  
 OY 1 MANKYSEILNIIILKRTKDNKLDLSGAKVYDVGVDELNKNKQFLTSSANSKIRV 60  
 DB 656 MANKYSEILNIIILKRTKDNKLDLSGAKVYDVGVDELNKNKQFLTSSANSKIRV 615  
 OY 61 TONONTNPNVDFSVFWRPKYKNDGIONTHRETTINMKNNSDKISIGNR 120  
 DB 716 TONONTNPNVDFSVFWRPKYKNDGIONTHRETTINMKNNSDKISIGNR 120  
 OY 121 IWLIDNKNSTKSVFVFNEDISYINMFWFVITNNANNTYINKNLESTNID 180  
 DB 776 IWLIDNKNSTKSVFVFNEDISYINMFWFVITNNANNTYINKNLESTNID 180  
 OY 181 REVANKEIFKLDIDTDFNMKYSIFMTELSGNSIERKYSISETYKLPMPN 240  
 DB 896 REVANKEIFKLDIDTDFNMKYSIFMTELSGNSIERKYSISETYKLPMPN 240  
 OY 241 LMKNTYTFMAGNKSITKADKSPVGLTRKYNKNSKYNVDTLCEKTFIRKS 300  
 DB 896 LMKNTYTFMAGNKSITKADKSPVGLTRKYNKNSKYNVDTLCEKTFIRKS 300  
 OY 301 NSGQNDQVYKEDYTLDFNNQKRWYTYKFKKEKFLAPISDSSELYNTQIK 360  
 DB 956 NSGQNDQVYKEDYTLDFNNQKRWYTYKFKKEKFLAPISDSSELYNTQIK 360  
 OY 361 EYDQTFQKQIFKDESDTDLGIGHRTFSGVYKVKYKFLAPISDSDEFYTIQIK 420  
 DB 1016 EYDQTFQKQIFKDESDTDLGIGHRTFSGVYKVKYKFLAPISDSDEFYTIQIK 420  
 OY 421 YNKLGNQWTFPDEWTE 440  
 DB 1076 YNKLGNQWTFPDEWTE 1095  
 RESULT 9  
 US-09-831-050-42  
 Sequence 42, Application 3C/US9715194  
 GENERAL INFORMATION:  
 APPLICANT: Williams, James A.  
 INVENTOR: Williams, James A.  
 TITLE OF INVENTION: Multivalent Vaccine For Clostridium  
 TITLE OF INVENTION: Botulinum Neurotoxin  
 NUMBER OF SEQ IDS NOS: 22  
 SOFTWARE: Patent In Ver. 2.1  
 ADDRESS: Medien & Carroll  
 STREET: 220 Montgomery Street, Suite 2200  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM:  
 MEDIAN TYPE: Floppy disk  
 COMPUTER: IBM PC compatible





GENERAL INFORMATION:  
 APPLICANT: Middlebrook, John I.  
 APPLICANT: Lapeotiere, Hugh F.  
 APPLICANT: Lapeotiere, Hugh F.  
 APPLICANT: Brown, Douglas R.  
 TITLE OF INVENTION: POLYPEPTIDE FUSION PRODUCT AS VACCINE  
 NUMBER OF SEQUENCES: 1  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John F. Moran  
 ADDRESSEE: John F. Moran  
 CITY: Fredrick  
 STATE: Maryland  
 COUNTRY: US  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 FILING DATE: 15-Oct-2002  
 APPLICATION NUMBER: US/08/271,012  
 PRIOR APPLICATION NUMBER: US/08/271,012  
 ATOM-BUILDING DATE: 08/04/2004  
 NAME: Ingolia, Diane E.  
 REGISTRATION NUMBER: 40-027  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 TELEFAX: (415) 397-8338  
 INFORMATION DATE: 08/04/2004  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
 us-09-910-186a-8.rapm  
 1 MARYNSLNNILNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 60  
 852 MFKNTSESLNHLNLYKONNLDLSGKGVYGVDELNKKKFLTSANSKIRV 911  
 61 TONKINSPVYGVDELNKKKFLTSANSKIRV 120  
 912 TONKINSPVYGVDELNKKKFLTSANSKIRV 180  
 121 TWLTDNKKKFLTSANSKIRV 240  
 972 TWLTDNKKKFLTSANSKIRV 300  
 181 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 360  
 1032 REVANGELIFKLDLDDTDFOTWMTYFVFNELSSONKIRV 420  
 241 LAMNRYTFVFNELSSONKIRV 480  
 1092 LAMNRYTFVFNELSSONKIRV 540  
 301 NGSNDVWVDELNKKKFLTSANSKIRV 600  
 1152 NGSNDVWVDELNKKKFLTSANSKIRV 660  
 361 EYDQSPVYGVDELNKKKFLTSANSKIRV 720  
 1212 EYDQSPVYGVDELNKKKFLTSANSKIRV 780  
 421 YKALQKQVYGVDELNKKKFLTSANSKIRV 840  
 1272 YKALQKQVYGVDELNKKKFLTSANSKIRV 900

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1291 amino acids  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear









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; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; APPLICANT: Lynn Donette-Stamm et al
; CURRENT FILING DATE: 1997-08-14
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; LENGTH: 5676
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-4751

Query Match 4.94; Score 114.5; DB 6; Length 3636;
Best Local Similarity 32.47; pred. No. 1.6;
Matches 99; Conservative 78; Mismatches 158; Indels 151; Gaps 27;

OY 2 ANKYSREILNIIILALVYKRN...IDLSGTARVYEDV...--LAKNK--...FLITS 53
DQ 264 ADENYCAIDNVALGR...KGNPDNHC...--FNGI EKESYNSILFSEFMIA 316
QY 54 ANK...--THVIGNTONTFNSVLDPSVETPRKNDI...--QNTFNP 98
DQ 317 NKRGQTOVLNANRKE...ASTDGGVYRFLKP...--DNVHRKYQVFPNHEID 372
QY 99 ...--YTLNKKNSKMSIKRHNRL...LNDIGKTSVYFPIR...EDI 144
DQ 373 FRQIDGJGYTSF...DIDGNSGRHYKSVKQNV...--KNGE...--FEVFRIZEN 426
QY 145 SEI...--NHRFVITNN...--NNKTI-YINGKLENT...--DKDIEVYANGSI 189
DQ 427 ONFAAA...QNGEYKATYKFEVYDNTSEVNSTVNGVGNSTVNSPVYFTRD...--NHTL 483
QY 130 IFKLD...--DIDKQDFMKKYSFNTLSQSN...--EERIKQSYBEL 233
DQ 234 ...--KDFNGENL...--YKKEY...--YFNAGKNSYIKLKDSVPVE 269
QY 484 FTSMLNAGRAUDVR...FUPNKLIM...--HYLQVWISFVETVFNALATFSEIT 540
DQ 541 INTNDYVTCQYTPS...YINNKEDLSQVWIIIFPSNVLASVYKNGRERAPVIZ 600
QY 270 ILRSYKNSKNTINRD...LYTGKFIIRKSSQSDINDIVKMDYIYDFPNMQR 328
DQ 601 ETNTPPNQRYSGQLDELQELTINRYNSAREINDNAGMDVAT...DSTLFTZ... 657
DQ 329 VYVYKPKKEEKLAPLSDSELENLTQKTDSDQYPTVSCOLLFKDSEDTGLIG 386
DQ 658 ...--SKOTVDQIDENKSIENSI...--DQELTD...--G 685
QY 389 THWFTSEGI 397
DQ 686 VERVEAQL 694

RESULT 5
; Sequence 2890
; ORGANISM: Staphylococcus epidermidis
; APPLICANT: Lynn Donette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; PRIOR FILING DATE: 1997-08-14
; CURRENT FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; LENGTH: 5676
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-4751

Query Match 4.94; Score 114.5; DB 6; Length 3636;
Best Local Similarity 32.47; pred. No. 1.6;
Matches 99; Conservative 78; Mismatches 158; Indels 151; Gaps 27;

OY 2 ANKYSREILNIIILALVYKRN...IDLSGTARVYEDV...--LAKNK--...FLITS 53
DQ 264 ADENYCAIDNVALGR...KGNPDNHC...--FNGI EKESYNSILFSEFMIA 316
QY 54 ANK...--THVIGNTONTFNSVLDPSVETPRKNDI...--QNTFNP 98
DQ 317 NKRGQTOVLNANRKE...ASTDGGVYRFLKP...--DNVHRKYQVFPNHEID 372
QY 99 ...--YTLNKKNSKMSIKRHNRL...LNDIGKTSVYFPIR...EDI 144
DQ 373 FRQIDGJGYTSF...DIDGNSGRHYKSVKQNV...--KNGE...--FEVFRIZEN 426
QY 145 SEI...--NHRFVITNN...--NNKTI-YINGKLENT...--DKDIEVYANGSI 189
DQ 427 ONFAAA...QNGEYKATYKFEVYDNTSEVNSTVNGVGNSTVNSPVYFTRD...--NHTL 483
QY 130 IFKLD...--DIDKQDFMKKYSFNTLSQSN...--EERIKQSYBEL 233
DQ 234 ...--KDFNGENL...--YKKEY...--YFNAGKNSYIKLKDSVPVE 269
QY 484 FTSMLNAGRAUDVR...FUPNKLIM...--HYLQVWISFVETVFNALATFSEIT 540
DQ 541 INTNDYVTCQYTPS...YINNKEDLSQVWIIIFPSNVLASVYKNGRERAPVIZ 600
QY 270 ILRSYKNSKNTINRD...LYTGKFIIRKSSQSDINDIVKMDYIYDFPNMQR 328
DQ 601 ETNTPPNQRYSGQLDELQELTINRYNSAREINDNAGMDVAT...DSTLFTZ... 657
DQ 329 VYVYKPKKEEKLAPLSDSELENLTQKTDSDQYPTVSCOLLFKDSEDTGLIG 386
DQ 658 ...--SKOTVDQIDENKSIENSI...--DQELTD...--G 685
QY 389 THWFTSEGI 397
DQ 686 VERVEAQL 694

RESULT 6
; Sequence 2890
; ORGANISM: Staphylococcus epidermidis
; APPLICANT: Lynn Donette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; PRIOR FILING DATE: 1997-08-14
; CURRENT FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; LENGTH: 5676
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-2890

Query Match 4.74; Score 111; DB 6; Length 321;
Best Local Similarity 19.74; pred. No. 1.2;
Matches 71; Conservative 72; Mismatches 120; Indels 98; Gaps 20;
OY 47 LSSANSKRY...--TONUNIFNSYFLDVS...--PWIRI 83

```









Query Match  
Initiability 4.44; Score 104.5; DB 6; Length 406;  
Matches 60; Conservative 4; Mismatches 87; Idicals 91; Gaps 15)

Oy 151 WPTNENKAKITNKKENSDNDKIDREVIANGELI-----IKR 152  
Db 32 NINQENAVYTK-----YFKKEELPLASDELYWIOIK--EYGEPTTSCQ 371  
Oy 183 LQDIDQDQPTKMYISIFNLESG-SHIEETKIGTSEIKEDKQKQKAKNMYTWN 251  
Db 470 NLETKNLEIKRSLSTHSTENKIPGIISSIFSTFVFNLSUCHNITNGSTIPQ 539  
Oy 70 EASDITKEPNEQVNFARVCOQNSDQARISKPT-LALF-ENQUMKSEY----- 123  
Db 232 AQEN-----SYKLAKDSFVEI-----LTKSK-----YNSKSNYEDIGEX 293  
Oy 124 RQSKYKAKITQKQSDQDQETROLAETTLQSKRNKICQDQKQDNFT----- 176  
Oy 294 FIKRSENGSINDVAKEDYILDYFNFNUNENAVIT-----YK-YFKKEELKLAP 347  
Db 177 -YFVRYN-----LQSDQKJAGQDSEYKVEYKQSHHITFQSHKSNFQWYLOM 227  
Oy 348 SOSSELTWIKIKETQETQST-----OLFKKDESTDE 383  
Db 228 TRDVTWIKWQK-----CVPLEITFETPSEHETEE 259

RESULT 15  
US-10-092-411A-2972  
Sequence 2972; Application US/10092411A  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 032796-101  
CURRENT APPLICATION NUMBER: US/10/092-411A  
PRIORITY FILING DATE: 2002-07-07  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064-964  
PRIOR APPLICATION NUMBER: US 60/055-779  
PRIOR FILING DATE: 1997-08-14  
PRIOR FILING DATE: 1997-08-14  
SEQ ID NO: 5676  
SEQ ID NO: 2972  
LENGTH: 570  
TYPE: PRT  
SOURCE: Staphylococcus epidermidis  
US-10-092-411A-2972

Query Match 4.44; Score 102.5; DB 6; Length 570;  
Best Local Similarity 19.64; Pred. No. 6.11;  
Matches 91; Conservative 74; Mismatches 118; Idicals 165; Gaps 25;

Oy 2 ANKYNSTLNNHILNLEYKQNNLID-SQYKAVYUQ--YE--LND-----KNQK 49  
Db 39 ATYTHPQMLKVL-----YATQVTSKRIEKLNDSTROMHISQK-K 83  
Oy 105 LTESANKITQKQNNIFNVLDFSVFPIKQKQNTQWTHNETINCKNS 109  
Db 84 PEKTIQWVWYKALLESIFQ-----TQCVKQNNLIDKATD----- 127  
Oy 110 QKISQIRG--LWTL-----IDNKAKTSFVEY-----NIEDISYINHFV 154  
Db 128 OTLNNANRYTPNKAQSTONKESKASQALWELVTKITPLEIDHD----- 178  
Oy 155 TTNLNNAKITNGKLENDIKQKRIANGELIFKQDIDQFQTKNKISFTE 214  
Db 179 ---NEILKEIDGLS-HLWDEIKENINCK-----GK 211  
Oy 215 LQSNIEETKQTSYKACQWQNLATNRYWPKAKNRYKAKKQSV----- 267  
Oy 212 THQKRLKQKIKYKQNDVFN--KTYEPOQSLDKNSYKTDATFMHMEZ 269  
Db 266 ---GELLTSEKYN--QNSVYKIDLY-----GGE-----KFLIR-- 297  
Oy 270 MKNQGL--EPQNLQATQNSVPLVSTQYPTQPTMIFPLNSIQTYQVPIY 374  
Db 298 ---KNSHSQNDINVKEDYITLDQFNLOBRVYTKYFKEELKFLAP-ESSE 354  
Oy 328 GQGESKATLIDQFMT-----LITQWTKATY-----KSDIF 366  
Oy 355 NTKQKYTE-QPTSC-----OLFKKDESTDEGLCHREYE 394  
Db 367 WT-QNSHDEIDQFQPNKQKQKAFKAYINDQKQKFLITE 410

Search completed November 1, 2002, 08:33:23

Fri Nov 1 18:34:11 2002

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Job time : 14 secs

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